

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:25:34 ; Search time 93.7758 Seconds
(without alignments)
7048.158 Million cell updates/sec

Title: US-10-029-436-1_COPY_61_1251
Perfect score: 1191
Sequence: 1 atgtggaacagctctgacgc.....gtttccataggctccattag 1191

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents,NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1191	100.0	1498	2	US-08-775-428-1
2	87.8	7.4	1382	4	US-09-364-425B-22
3	87.8	7.4	1584	1	US-08-748-485-2
4	87.8	7.4	1584	4	US-09-016-434-284
5	87	7.3	2481	1	US-08-467-568-1
6	87	7.3	2481	2	US-09-030-582-1
7	87	7.3	2481	5	PCT-US94-09051-1
8	83	7.0	921	1	US-08-722-001-17
9	83	7.0	1567	1	US-08-722-001-24
10	83	7.0	1738	1	US-08-334-698-3
11	83	7.0	1738	1	US-08-228-932-3
12	83	7.0	1738	1	US-08-468-939-3
13	83	7.0	1738	2	US-08-406-855A-3
14	83	7.0	1738	2	US-08-722-190-3
15	83	7.0	1738	3	US-08-244-354-3
16	83	7.0	1738	3	US-09-206-899-3
17	83	7.0	1738	4	US-09-444-783-3
18	83	7.0	1738	4	US-09-688-415-3
19	83	7.0	1738	4	US-09-016-434-1402
20	83	7.0	1738	4	US-09-444-783-3
21	83	7.0	1738	5	PCT-US95-04203-3
22	80	6.7	1092	3	US-09-077-675A-15
23	80	6.7	1092	4	US-09-077-674-15
24	80	6.7	3129	3	US-09-077-675A-14
25	80	6.7	3129	4	US-09-077-674-14
26	78.4	6.6	1095	4	US-09-743-475-2
27	78.4	6.6	4009	4	US-09-743-475-1

28	75	6.3	1088	3	US-09-077-675A-6	Sequence 6, Appli
29	75	6.3	1088	4	US-09-077-674-6	Sequence 6, Appli
30	75	6.3	1101	4	US-09-016-434-1148	Sequence 1148, Ap
31	75	6.3	1101	4	US-09-170-496D-87	Sequence 87, Appl
32	75	6.3	1101	4	US-09-170-496D-209	Sequence 209, App
33	75	6.3	1101	4	US-09-364-425B-44	Sequence 44, Appli
34	75	6.3	1122	3	US-09-077-675A-9	Sequence 9, Appli
35	75	6.3	1122	4	US-09-077-674-9	Sequence 9, Appli
36	73.6	6.2	1050	4	US-09-762-661A-1	Sequence 1, Appli
37	70.2	5.9	7218	1	US-08-232-463-14	Sequence 14, Appl
38	70	5.9	1080	3	US-08-875-540-14	Sequence 14, Appl
39	70	5.9	1080	4	US-09-473-634-14	Sequence 14, Appl
40	69.8	5.9	1601	1	US-08-722-001-7	Sequence 7, Appli
41	69.8	5.9	1639	1	US-08-334-698-5	Sequence 5, Appli
42	69.8	5.9	1639	1	US-08-228-932-5	Sequence 5, Appli
43	69.8	5.9	1639	1	US-08-468-939-5	Sequence 5, Appli
44	69.8	5.9	1639	2	US-08-406-855A-5	Sequence 5, Appli
45	69.8	5.9	1639	2	US-08-722-190-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-775-428-1
; Sequence 1, Application US/08775428
; Patent No. 5976834
; GENERAL INFORMATION:
; APPLICANT: Sathe, Ganesh
; APPLICANT: Fuetterer, Wendy
; APPLICANT: Bergsma, Derk
; APPLICANT: Ellis, Catherine
; TITLE OF INVENTION: CDNA CLONE HNFJD15 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,428
; FILING DATE: 09-JAN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4060
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1498 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-775-428-1

Query Match 100.0%; Score 1191; DB 2; Length 1498;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTACCATGAGTCTGTGCTGGCTATCGT 60
Db	76 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTACCATGAGTCTGTGCTGGCTATCGT 135
QY	61 TATGTTGCAGTTAGCTGGGGGGTGGTGGTGTGTGACAGGCACCGTGGGCAATGTGCTC 120
Db	136 TATGTTGCAGTTAGCTGGGGGGTGGTGGTGTGTGACAGGCACCGTGGGCAATGTGCTC 195
QY	121 ACCCTACTGGCCTTGGCCATCCAGGCCCAAGTCCGTACCCGATTCAACCTGCTCATAGCC 180
Db	196 ACCCTACTGGCCTTGGCCATCCAGGCCCAAGTCCGTACCCGATTCAACCTGCTCATAGCC 255
QY	181 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTTCAGCCCTTCTCTGTGGACACC 240
Db	256 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTTCAGCCCTTCTCTGTGGACACC 315
QY	241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACAGGTATTTGGGCTCCTCCTT 300
Db	316 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACAGGTATTTGGGCTCCTCCTT 375
QY	301 TTGCTCCTCAATCTGTCTCCATCCTGACCTCTGCCTCATCGACCTGGGACGCTACCTC 360
Db	376 TTGCTCCTCAATCTGTCTCCATCCTGACCTCTGCCTCATCGACCTGGGACGCTACCTC 435
QY	361 CTCATTGCCCAACCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 420
Db	436 CTCATTGCCCAACCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 495
QY	421 CTGGTGAGCACTGGGTGTGGGGCTGGCCAGCTTTGCTCCCTCTGGCCTATTTATATC 480
Db	496 CTGGTGAGCACTGGGTGTGGGGCTGGCCAGCTTTGCTCCCTCTGGCCTATTTATATC 555
QY	481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTCACCGCATCCGAGCCGGCTTACACCA 540
Db	556 CTGGTACCTGTAGTCTGCACCTGCAGCTTTCACCGCATCCGAGCCGGCTTACACCA 615
QY	541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
Db	616 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 675
QY	601 ATCCACCGCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 660
Db	676 ATCCACCGCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 735
QY	661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATCCCTGGTCTGTTTCCAGGAG 720
Db	736 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATCCCTGGTCTGTTTCCAGGAG 795
QY	721 CTGGACAGCAGGTTAGCATCAGSAGGACCCAGTGAGGGGATTTCATCTGAGCCAGTCA 780
Db	796 CTGGACAGCAGGTTAGCATCAGSAGGACCCAGTGAGGGGATTTCATCTGAGCCAGTCA 855
QY	781 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
Db	856 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 915
QY	841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCCAAGCCA 900
Db	916 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCCAAGCCA 975
QY	901 ATTAAGGAGCCAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db	976 ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1035
QY	961 TGTGTTGCTGTGTTTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db	1036 TGTGTTGCTGTGTTTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1095
QY	1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCAACCTCACCTGG 1080
Db	1096 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCAACCTCACCTGG 1155

QY	1081 CTCAATGGTTGCATCAACCCCTGTCTCTATGAGCCCATGAACCCGCAATTCGCGCAAGCA 1140
Db	1156 CTCAATGGTTGCATCAACCCCTGTCTCTATGAGCCCATGAACCCGCAATTCGCGCAAGCA 1215
QY	1141 TATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db	1216 TATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 1266
RESULT 2	
US-09-364-425B-22	
; Sequence 22, Application US/09364425B	
; Patent No. 6653086	
; GENERAL INFORMATION:	
; APPLICANT: Behan, Dominic P.	
; APPLICANT: Chalmers, Derek T.	
; APPLICANT: Liaw, Chen W.	
; APPLICANT: Lin, I-Lin	
; APPLICANT: Lowitz, Kevin P.	
; APPLICANT: Chen, Ruoping	
; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor	
; FILE REFERENCE: Aren0047	
; CURRENT APPLICATION NUMBER: US/09/364,425B	
; CURRENT FILING DATE: 2001-12-18	
; PRIOR APPLICATION NUMBER: 60/094,879	
; PRIOR FILING DATE: 1998-07-31	
; PRIOR APPLICATION NUMBER: 60/106,300	
; PRIOR FILING DATE: 1998-10-30	
; PRIOR APPLICATION NUMBER: 60/110,906	
; PRIOR FILING DATE: 1998-12-04	
; PRIOR APPLICATION NUMBER: 60/121,851	
; PRIOR FILING DATE: 1999-02-26	
; NUMBER OF SEQ ID NOS: 60	
; SOFTWARE: PatentIn version 3.1	
; SEQ ID NO 22	
; LENGTH: 1382	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
US-09-364-425B-22	
Query Match 7.4%; Score 87.8; DB 4; Length 1382;	
Best Local Similarity 53.7%; Pred. No. 7.3e-15;	
Matches 182; Conservative 0; Mismatches 157; Indels 0; Gaps 0;	
QY	100 GGCACCGCTGGGCAATGTCTCAGCAACCTCACACTGGCTGATCTCTACTGCACGCTCCTT 159
Db	181 GTCTGCTGGGAAACCTGGTCTATCGTGTGTCACCTTGTACAAAGTCTCTACCTCCTCACC 240
QY	160 CGATTCAACCTGCTCATAGCAACCTCACACTGGCTGATCTCTACTGCACGCTCCTT 219
Db	241 CTCAGCAACAAGTTCGTCTTCAGCCTGACTCTGTCCAACCTTCTGTCTGCTGCTGGTG 300
QY	220 CAGCCTTCTCTGTGGACACCTACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGC 279
Db	301 CTGCTTTTGTGGTGACGAGTCCATCCGAGGGAATGGATCTTTGGTGTAGTGTGGTG 360
QY	280 AGGTTATTGGGCTCCTCCTTTTGGCTCCAAATTCCTCTCCATCTCTGACCTCTGCTC 339
Db	361 AACTTCTCTGCCCTCCTCTACCTGCTGATCAGCTTGCAGCATGTAAACCTCGGGGTC 420
QY	340 ATCCGACTGGGACGCTACCTCTCATTTGCCACCTTAAGCTTTTCCCAAGTTTTCAGT 399
Db	421 ATTGCCATCGACCGCTACTATGCTGTCTGTACCCCATGGTGTACCCCATGAAGATCACA 480
QY	400 GCCAAGGGGATAGTGTGGCACTGGTGAGCACTGGGTT 438
Db	481 GGAACCGGGCTGTGATGGCACTTGTCTACATCTGGCTT 519

RESULT 3
US-08-748-485-2
; Sequence 2, Application US/08748485

QY 400 GCCAAGGGGATAGTGTGGCACTGGTGAGCACCTGGTT 438
 Db 587 GGAACCGGGCTGATGGCACTTGTCTACATCTGGCTT 625

RESULT 5
 US-08-467-568-1
 ; Sequence 1, Application US/08467568
 ; Patent No. 5817477
 ; GENERAL INFORMATION:
 ; APPLICANT: SOPPET, DANIEL R
 ; TITLE OF INVENTION: ADRENERGIC RECEPTOR
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
 ; ADDRESSEE: Stewart & Olstein
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07068-1739
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467,568
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferraro, Gregory D
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-324
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2481 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 101..1687
 US-08-467-568-1

Query Match 7.3%; Score 87; DB 1; Length 2481;
 Best Local Similarity 53.7%; Pred. No. 1.6e-14;
 Matches 180; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
 QY 104 CCGTGGGCAATGTGCTCACCCTACTGGCCCTGGCCATCCAGCCCAAGCTCCGTACCCGAT 163
 Db 225 CCTGGGAAACCTGGTCATCGTGGTCACCTTGACAGAAGTCTCCTACCTCCTCACCTCA 284
 QY 164 TCAACCTGCTCATAGCAACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGC 223
 Db 285 GCAACAAGTTCTGCTTTCAGCCTGACTCTGTCCAACTTCTGCTGTCCGTGTTGGTGCTGC 344
 QY 224 CCTTCTCTGTGGACACCTACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGG 283
 Db 345 CTTTGTGGTGACGAGCTCCATCCGAGGGAATGGATCTTTGGTGTAGTGTGGTCAACT 404
 QY 284 TATTGGGCTCCTCCTTTTGGCCTCCAATTCTGTCTCCATCTGACCTCTGCCTCATCG 343
 Db 405 TCTCTGCCCTCCTTACCTGCTGATCAGCTTGTCCAGCATGTACCCATGTAACCCCTCGGGTCA 464
 QY 344 CACTGGGACGCTACCTCCTCATATTGCCACCCCAAGCTTTTCCCAAGTTTTCAGTGCCA 403
 Db 465 CCATCGACCGCTACTATGCTGTCTGTACCCCATGGTGTACCCCATGAAGATCACAGGGA 524

QY 404 AGGGGATAGTGTGGCACTGGTGAGCACCTGGTT 438
 Db 525 ACCGGGCTGTGATGGCACTTGTCTACATCTGGCTT 559

RESULT 6
 US-09-030-582-1
 ; Sequence 1, Application US/09030582
 ; Patent No. 5994506
 ; GENERAL INFORMATION:
 ; APPLICANT: SOPPET, DANIEL R
 ; TITLE OF INVENTION: ADRENERGIC RECEPTOR
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
 ; ADDRESSEE: Stewart & Olstein
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07068-1739
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/030,582
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/467,568
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferraro, Gregory D
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-324
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2481 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 101..1687
 US-09-030-582-1

Query Match 7.3%; Score 87; DB 2; Length 2481;
 Best Local Similarity 53.7%; Pred. No. 1.6e-14;
 Matches 180; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
 QY 104 CCGTGGGCAATGTGCTCACCCTACTGGCCCTGGCCATCCAGCCCAAGCTCCGTACCCGAT 163
 Db 225 CCTGGGAAACCTGGTCATCGTGGTCACCTTGACAGAAGTCTCCTACCTCCTCACCTCA 284
 QY 164 TCAACCTGCTCATAGCAACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGC 223
 Db 285 GCAACAAGTTCTGCTTTCAGCCTGACTCTGTCCAACTTCTGCTGTCCGTGTTGGTGCTGC 344
 QY 224 CCTTCTCTGTGGACACCTACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGG 283
 Db 345 CTTTGTGGTGACGAGCTCCATCCGAGGGAATGGATCTTTGGTGTAGTGTGGTCAACT 404
 QY 284 TATTGGGCTCCTCCTTTTGGCCTCCAATTCTGTCTCCATCTGACCTCTGCCTCATCG 343
 Db 405 TCTCTGCCCTCCTTACCTGCTGATCAGCTTGTCCAGCATGTACCCATGTAACCCCTCGGGTCA 464

QY 344 CACTGGGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCA 403
Db 465 CCAATCGACCGCTACTATGCTGCTGTACCCCATGGTGTACCCCATGAAGATCACAGGGA 524
QY 404 AGGGGATAGTGTGGCACTGGTGAGCACCTGGGTT 438
Db 525 ACCGGGCTGTGATGGCACTTGTCTACATCTGGCTT 559

RESULT 7
PCT-US94-09051-1
; Sequence 1, Application PC/TUS9409051
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Adrenergic Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09051
; FILING DATE: Submitted herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2481 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
PCT-US94-09051-1

Query Match 7.3%; Score 87; DB 5; Length 2481;
Best Local Similarity 53.7%; Pred. No. 1.6e-14;
Matches 180; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
QY 104 CCGTGGGCAATGTGCTCACCCCTACTGGCCCTTGGCCATCCAGCCCAAGCTCCGTAACCGAT 163
Db 225 CCTGGGAAACCTGGTCAATCGTGGTCACCTTGTACAGAAGTCTTACCTCCTCACCCCTCA 284
QY 164 TCAACCTGCTCATAGCCAACTCACACTGGCTGATCTCTCTACTGACAGCTCTCTCAGC 223
Db 285 GCAACAAGTTCGTCTTACGCCCTGACTCTGTCCAACTTCTGCTGTCGGTGTGGTGTGC 344
QY 224 CCTTCTGTGTGGACACCTACCTCACCTGCACTGGGGACCGGTGCCACCTTCTGCAGGG 283
Db 345 CTTTTGTGTGACGAGCTCCATCCGACGGGAATGGATCTTTGGTGTAGTGTGGTGCACACT 404
QY 284 TATTGGGCTCCTCCTTTTGGCTCCAATTCTGTCTCCATCTGACCTCTGCTCATCG 343
Db 405 TCTCTGCCCTCCTCTACCTGTGATCAGCTCTGCCAGCATGCTAACCCCTCGGGGTCAATTG 464
QY 344 CACTGGGACGCTACCTCCTCATTTGCCCAACCTTAAGCTTTTTCCTCAAGTTTTCAGTGCCA 403

Db 465 CCATCGACCGCTACTATGCTGCTGTACCCCATGGTGTACCCCATGAAGATCACAGGGA 524
QY 404 AGGGGATAGTGTGGCACTGGTGAGCACCTGGGTT 438
Db 525 ACCGGGCTGTGATGGCACTTGTCTACATCTGGCTT 559

RESULT 8
US-08-722-001-17
; Sequence 17, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHALC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19169Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-722-001-17

Query Match 7.0%; Score 83; DB 1; Length 921;
Best Local Similarity 52.1%; Pred. No. 1.4e-13;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
QY 100 GGCACCGTGGGCAATGTGCTCACCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACC 159
Db 183 GCCATCGTGGGCAACATCCTAGTCATCTTGTCTGTGGCTTGCACCGCACCTGCGGACG 242
QY 160 CGATTCAACCTGCTCATAGCCAACTCACACTGGTGTGATCTCTCTACTGCACGCTCCTT 219
Db 243 CCCACCACTACTTTCATTGTCAACCTGGCCATGGCCGACCTGCTGTGAGCTTACCCGTC 302
QY 220 CAGCCCTTCTCTGTGGACACCTACCTCCACCTGCACTGGGGACCGGTGCCACCTTCTGC 279
Db 303 CTGCCCTTCTCAGCGGCCCTAGAGGTGCTCGGCTACTGGGTGCTGGGGCGGATCTTCTGT 362

QY 280 AGGGTATTGGGCTCCTCTTTTGGCTCCAAATCTGTCTCCATCCTGACCCCTCTGCCTC 339
 Db 363 GACATCTGGGACCGGTGGATGCTGTGTGTCACAGCGTCCATCTGAGCCCTGTGCGCC 422
 QY 340 ATCGACTGGGACGCTACCTCTCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGT 399
 Db 423 ATCTCCATCGATCGTACATCGGGTGGCTACTCTCTCAGTATCCACAGTGGTCAAC 482
 QY 400 GCCAAGGGGATAGTGTGGCACTGGTGAGCACCTGGGTGTGGCGTGGCCAGCT 454
 Db 483 CGGAGGAAGGCCATCTTGGCCCTGCTCAGTGTCTGGGTCTTGTCCACCGTCACT 537

RESULT 9
 US-08-722-001-24
 ; Sequence 24, Application US/08722001
 ; Patent No. 5760054
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Wayne J.
 ; APPLICANT: Huff, Joel R.
 ; APPLICANT: Nerenberg, Jennie B.
 ; APPLICANT: Lee, Hee-Yoon
 ; APPLICANT: Bell, Ian M.
 ; TITLE OF INVENTION: ALPHA1C ADRENERGIC RECEPTOR ANTAGONISTS
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merck & Co., Inc.
 ; STREET: 126 Lincoln Avenue
 ; CITY: Rahway
 ; STATE: New Jersey
 ; COUNTRY: United States of America
 ; ZIP: 07065

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/722,001
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION NUMBER: 08/229,276
 FILING DATE: 14-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Appollina, Mary A.
 REGISTRATION NUMBER: 34,087
 REFERENCE/DOCKET NUMBER: 19169Y
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908)594-3462
 TELEFAX: (908)594-4720
 TELEX: 138825
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1567 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

US-08-722-001-24
 Query Match 7.0%; Score 83; DB 1; Length 1567;
 Best Local Similarity 52.1%; Pred. No. 1.7e-13;
 Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
 QY 100 GGCACCGTGGGCAATGTGCTCACCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACC 159
 Db 183 GCCATCGTGGGCAACATCCTAGTCACTTGTGTGGCTGTGCAACCGGCACCTGCGGACG 242
 QY 160 CGATTCAACCTGCTCATAGCCCAACCTCACACTGGCTGATCTCTTACTGACGCTCCTT 219

Db 243 CCCACCAACTACTTTCATTTGCAACCTGGCCATGGCCGACCTGCTGTTGAGCTTCACCGTC 302
 QY 220 CAGCCCTTCTCTGTGGACACCTACCTCCACCTGACCTGGCGCACCGGTGCCACCTTCTGC 279
 Db 303 CTGCCCTTCTCAGCGGCCCTAGAGGTGCTCGGCTACTGGGTGCTGGGCGGATCTTCTGT 362
 QY 280 AGGGTATTGGGCTCCTCTTTTGGCTCCAAATCTGTCTCCATCCTGACCCCTCTGCCTC 339
 Db 363 GACATCTGGGACCGGTGGATGCTGTGTGTCACAGCGTCCATCTGAGCCCTGTGCGCC 422
 QY 340 ATCGCACTGGGACGCTACCTCTCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGT 399
 Db 423 ATCTCCATCGATCGTACATCGGGTGGCTACTCTCTCAGTATCCACAGTGGTCAAC 482
 QY 400 GCCAAGGGGATAGTGTGGCACTGGTGAGCACCTGGGTGTGGCGTGGCCAGCT 454
 Db 483 CGGAGGAAGGCCATCTTGGCCCTGCTCAGTGTCTGGGTCTTGTCCACCGTCACT 537

RESULT 10
 US-08-334-698-3
 ; Sequence 3, Application US/08334698
 ; Patent No. 5556753
 ; GENERAL INFORMATION:
 ; APPLICANT: Jonathan A. Bard et al.
 ; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
 ; TITLE OF INVENTION: Receptors and Uses Thereof
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOPER & DUNHAM
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10112

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/334,698
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/952,798
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 376901
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEFAX: (212) 664-0525
 TELEX: (212) 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1738 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: N
 ANTI-SENSE: N
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 124..1683
 OTHER INFORMATION:
 US-08-334-698-3

Query Match 7.0%; Score 83; DB 1; Length 1738;
 Best Local Similarity 52.1%; Pred. No. 1.8e-13;

	Matches	185;	Conservative	0;	Mismatches	170;	Indels	0;	Gaps	0;
QY	100	GGCACCGTGGCAATGTGCTCACCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACC	159							
Db	298	GCCATCGTGGCAACAICCTAGTCACTTGTCTGTGGCCTGCAACCGGCACCTGCGGACG	357							
QY	160	CGATTCAACCTGCTCAAFAGCCAACTCACACTGGCTGATTCCTCTACTGCAAGCTCCCT	219							
Db	358	CCCAACCAACTACTTCATTGTCAACCTGGCCATGGCCGACCTGCTGTTGAGCTTCAACCGTC	417							
QY	220	CAGCCCTTCTCTGTGGACACCTACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCGTC	279							
Db	418	CTGCCCTTCTCAGCGGCCCTAGAGGTGCTCGGCTACTGGGTGCTGGGGCGGATCTTCTGT	477							
QY	280	AGGGTATTTGGGCTCCTCCTTTTGTGCTTCCAAATCTGTCTCCATCCTGACCCCTCTGCCCTC	339							
Db	478	GACATCTGGGCAGCCGTGGATGCTCTGTGCTGCACAGCGTCCATCTGAGCCCTGTGGGCC	537							
QY	340	ATCGCACTGGGACGGTACCTCCTCATTTGCCCAACCTAAGCTTTTCCCCAAGTTTTTCAGT	399							
Db	538	ATCTCCATCGATCGCTACATCGGGGTGCGTACTCTCTGCAGTATCCCACGCTGGTCACC	597							
QY	400	GCCAAGGGGATAGTCTGGCACTGGTGAGCACCTGGGTTGTGGGCGGTGGCCAGCT	454							
Db	598	CGGAGGAAGGCCATCTTGGCGCTGCTCAGTGTCTGGGTCTGTGCCACCGTCATCT	652							

RESULT 11
US-08-228-932-3
; Sequence 3, Application US/08228932
; Patent No. 5578611

```

;
;
; GENERAL INFORMATION:
;
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
; APPLICANT: Theresa A. Brancheck, John M. Wetzel and Paul R. Hartig
;
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
;
; TITLE OF INVENTION: PROSTATIC HYPERPLASIA
;

```

```
, ,  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:
```

```

;
US-08-228-932-3
OTHER INFORMATION:
Query Match      7.0%; Score 83; DB 1; Length 1738;
Best Local Similarity 52.1%; Pred. No. 1.8e-13;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 100 GGCACCGTGGGCAATGTGCTCACCTACTGGCCTTGSCCATCCAGCCCAAGCTCCGTACC 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 GCCATCGTGGGCAACATCCTAGTCATCTTGCTGTGGCTGCAACCGGCACCTGCGGACG 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 160 CGATTCAACCTGTCTCATAGCCAAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCIT 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 CCCACCAACTACTTCATTGTCAACCTGGCCATGGCCGACCTGCTGTTGAGCTTCACCGTC 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 220 CAGCCCTTCTCTGTGGACACCTACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGC 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 CTGCCCTTCTCAGCGGCCCTAGAGGTGCTCGGCTACTGGGTGCTGGGCGGATCTTCTGT 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 280 AGGGTATTTGGGCTCCTCCTTTTGGCCTCCAATCTGTCTTCCATCCTGACCCCTCTGCCCTC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 GACATCTGGGCGAGCCGTGGATGTCCTGTGCTGCACAGCGTCCATCTGAGCCTGTGCGCC 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 340 ATCGCACTGGGACGCTACCTCCTCATTTGCCCAACCTTAAGCTTTTTTCCCCAAGTTTTTCAGT 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 ATCTCCATCGATCGCTACATCGGGGTGGCTACTCTCTGAGTATCCCAACGCTGGTCACC 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 400 GCCAAGGGGATAGTGTGGCACTGGTGAGCACTGGGTGTGGCGGTGGCCAGCT 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 CGGAGGAAGGCCATCTTGGCGCTGCTCAGTGTCTGGGTCTTGTCCACCGTCACT 652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 12
US-08-468-939-3
; Sequence 3, Application US/08468939
; Patent No. 5714381
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof

10

```

;
; NAME/KEY: CDS
; LOCATION: 124..1683
; OTHER INFORMATION:
US-08-468-939-3

Query Match          7.0%; Score 83; DB 1; Length 1738;
Best Local Similarity 52.1%; Pred. No. 1.8e-13;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 100 GGCACCGTGGGCAATGCTCACCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACC 159
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||| ||| ||| ||| |||
Db 298 GCCATCGTGGGCAACATCTAGTCATCTTGTCTGTGGCTGCAACCGGCACCTGCGGACG 357

QY 160 CGATTCAACCTGCTCATAGCCAACTCACACTGGCTGATCTCCTCTACTGCACGCTCCTT 219
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 CCCACCAACTACTTCATTTCAACCTGGCCATGGCCGAGCTGCTGTGAGCTTTCACCGTC 417

QY 220 CAGCCCTTCTCTGTGGACACCTACCTCCACCTGCACCTGCCGCAACCGGTGCCACCTTTCG 279
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 418 CTGCCCTTCTCAGCGGCCCTAGAGGTGCTCGGCTACTGGGTGCTGGGCGGATCTTCTGT 477

QY 280 AGGGTATTTGGGCTCCTCCTTTTGGCTTCCAAATCTGTCTCCATCCTGACCCCTCTGCCTC 339
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 GACATCTGGGCAGCCGTGGATGTCTGTGTGCACAGCGTCCATCTGAGCCTGTGGGCC 537

QY 340 ATCGCACTGGGACGCTACCTCCTCATTTGCCCAACCCCTAAGCTTTTCCCAAGTTTTCAGT 399
      ||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 ATCTCCATCGATCGCTACATCGGGGTGCGTACTCTGCAATATCCCACGCTGGTCAC 597

QY 400 GCCAAGGGATAGTGTGGCACTGGTGAGCACCTGGGTGTGGCGGTGGCCAGCT 454
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 CGGAGGAAGGCCATCTTGGCGTGTGCTCAGTGTCTGGGTCTGTCCACCGTCATCT 652

```

RESULT 13
US-08-406-855A-3
; Sequence 3, Application US/08406855A
; Patent No. 5861309
; GENERAL-~~INFORMATION~~:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Durham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,855A
; FILING DATE: 21-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown

```

; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1683
; OTHER INFORMATION:
;
US-08-406-855A-3

Query Match          7.0%; Score 83; DB 2; Length 1738;
Best Local Similarity 52.1%; Pred. No. 1.8e-13;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0

QY 100 GGCACCGTGGGCAATGTCTCACCCCTACTGGCCCTTGGCCATCCAGCCCAAGCTCCGTACC 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 GCCATCGTGGGCAACATCCTAGTCATCTTGTCTGTGGCCTGCAACCGGCACCTTGGGACG 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 160 CGATTCAACCTGCTCATAGCAACCTCACACTGGCTGATCTCCTCTACTGACCGTCCTT 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 CCCACCAACTACTTTCATTGTCAACCTGGCCATGGCCGACCTGCTGTTGAGCTTCACCGTC 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 220 CAGCCCTTCTCTGTGGACACCTACCTCCACCTGCACCTGGCGCACCGGTGCCACTTCTGC 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 CTGCCCTTCTCAGCGGCCCTAGAGGTGCTCGGCTACTGGGTGCTGGGGCGGATCTTCTGT 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 280 AGGGTATTGGGCTCCTCCTTTTTCCTTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 GACATCTGGGCAGCCGTGGATGTCCTGTGCTGCACAGCGTCCATTCTGAGCCTGTGCGCC 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 340 ATCGCACTGGGACGCTACCTCTCTCATTGCCCCACCCCTAAGCTTTTCCCAAGTTTTCAGT 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 ATCTCCATCGATCGCTACATCGGGGTGCGCTACTCTCTGCAGTATCCACACGCTGGTCACC 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 400 GCCAAGGGGATAGTGTGGCACTGGTGAGCACTGGGTGTGGCGCTGGCCAGCT 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 CGAGGAAGGCCATCTTGGCGCTGCTCAGTGTCTGGGTCTTGTGCCACCGTCACT 652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 14
US-08-722-190-3
; Sequence 3, Application US/08722190
; Patent No. 5990128
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George
; APPLICANT: Chiu, Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,190
; FILING DATE: 4-APR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 08:34:21 ; Search time 29 Seconds
(without alignments)
704.962 Million cell updates/sec

Title: US-10-029-436-2
Perfect score: 2041
Sequence: 1 MNSSDANFSCYHESVLGYR.....FRQAYGSILKRGPRSFRLH 396

Scoring table: BLOSUM62
Gapop 10.0., Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2041	100.0	396	2	US-08-775-428-2
2	293	14.4	443	1	US-07-626-618A-18
3	293	14.4	443	1	US-08-333-977-18
4	291.5	14.3	515	1	US-08-194-338-3
5	290.5	14.2	515	4	US-09-688-415-10
6	288.5	14.1	515	1	US-08-444-734A-7
7	288.5	14.1	515	2	US-08-406-855A-22
8	288.5	14.1	515	3	US-09-206-899-22
9	287.5	14.1	515	4	US-09-688-415-9
10	286.5	14.0	515	1	US-08-722-001-25
11	286.5	14.0	517	2	US-08-467-568-10
12	286.5	14.0	517	2	US-09-030-582-10
13	285.5	14.0	444	1	US-07-626-618A-19
14	285.5	14.0	444	1	US-08-333-977-19
15	285.5	14.0	520	1	US-08-334-698-4
16	285.5	14.0	520	1	US-08-228-932-4
17	285.5	14.0	520	1	US-08-468-939-4
18	285.5	14.0	520	2	US-08-406-855A-4
19	285.5	14.0	520	2	US-08-722-190-4
20	285.5	14.0	520	3	US-08-244-354-4
21	285.5	14.0	520	3	US-09-206-899-4
22	285.5	14.0	520	4	US-09-444-783-4
23	285.5	14.0	520	4	US-09-688-415-4
24	285.5	14.0	520	4	US-09-444-783-4
25	285.5	14.0	520	5	PCT-US95-04203-4
26	285	14.0	513	2	US-08-406-855A-21
27	285	14.0	513	3	US-09-206-899-21

28	283.5	13.9	444	1	US-07-781-254A-1	Sequence 1, Appli
29	281.5	13.8	466	2	US-08-406-855A-23	Sequence 23, Appl
30	281.5	13.8	466	3	US-09-206-899-23	Sequence 23, Appl
31	281.5	13.8	466	4	US-09-688-415-11	Sequence 11, Appl
32	278.5	13.6	515	3	US-09-032-742-5	Sequence 5, Appli
33	278	13.6	375	1	US-08-118-270-17	Sequence 17, Appl
34	278	13.6	375	5	PCT-US93-08528-17	Sequence 17, Appl
35	278	13.6	443	1	US-08-444-734A-3	Sequence 3, Appli
36	274.5	13.4	353	2	US-08-467-559B-10	Sequence 10, Appl
37	274	13.4	429	2	US-08-748-485-7	Sequence 7, Appli
38	274	13.4	466	1	US-08-334-698-6	Sequence 6, Appli
39	274	13.4	466	1	US-08-228-932-6	Sequence 6, Appli
40	274	13.4	466	1	US-08-468-939-6	Sequence 6, Appli
41	274	13.4	466	1	US-08-722-001-12	Sequence 12, Appl
42	274	13.4	466	1	US-08-722-001-28	Sequence 28, Appl
43	274	13.4	466	2	US-08-467-568-11	Sequence 11, Appl
44	274	13.4	466	2	US-08-406-855A-6	Sequence 6, Appli
45	274	13.4	466	2	US-08-722-190-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-775-428-2
; Sequence 2, Application US/08775428
; Patent No. 5976834
; GENERAL INFORMATION:
; APPLICANT: Sathe, Ganesh
; APPLICANT: Fuetterer, Wendy
; APPLICANT: Bergsma, Derk
; APPLICANT: Ellis, Catherine
; TITLE OF INVENTION: CDNA CLONE HNFJD15 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,428
; FILING DATE: 09-JAN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4060
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-775-428-2

Query Match 100.0%; Score 2041; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 7.3e-176;

Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWSSDANFSCYHESVLGYRYVAVSWGVAVTGTGVTNLTLLALAIQPKLRFNLLIA 60
Db 1 MWSSDANFSCYHESVLGYRYVAVSWGVAVTGTGVTNLTLLALAIQPKLRFNLLIA 60

QY 61 NLTLADLLYCTLLQPFSDVDTYLHLHWRGTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
Db 61 NLTLADLLYCTLLQPFSDVDTYLHLHWRGTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120

QY 121 LIAHPKLPQVFSAGKIVLALVSTWVVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSAGKIVLALVSTWVVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180

QY 181 ILMGIYFVLGLSSVGIFCYLIHQVKRAAALDQYKLRQASIHNSHVARTDEAMPGRFQE 240
Db 181 ILMGIYFVLGLSSVGIFCYLIHQVKRAAALDQYKLRQASIHNSHVARTDEAMPGRFQE 240

QY 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
Db 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300

QY 301 IKGARRAPDSSSEFGKVTRMCFVLCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSSEFGKVTRMCFVLCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360

QY 361 LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 2

US-07-626-618A-18

; Sequence 18, Application US/07626618A

; Patent No. 5422265

; GENERAL INFORMATION:

; APPLICANT: Van Tol, Hubert H.M.

; APPLICANT: Civelii, Olivier

; TITLE OF INVENTION: A No. 5422265e1 Human Dopamine Receptor and Uses

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Allegretti & Witcoff, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/626,618A

; FILING DATE: 7 DEC 1990

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5422265nan, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 90,1092

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

; TELEX: 810-221-8317

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 443 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

US-07-626-618A-18

Query Match 14.4%; Score 293; DB 1; Length 443;

Best Local Similarity 25.9%; Pred. No. 2.8e-18;

Matches 115; Conservative 66; Mismatches 179; Indels 84; Gaps 16;

QY 2 WNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGVTNLTLLALAIQPKLRFNLLIAN 61
Db 22 FNGSDGKADRPH-----YHYATLLTLLIAVI-VFENVLCMAVSREKALQTTNYLIVS 75

QY 62 LTLADLLYCTLLQPFSDVDTYLHL--HWRTGATFCRVFGLLLFASNSVSILTCLIALGRY 119
Db 76 LAVADLLVATLVMPWV--YLEVVGEWKFSRIHCDIFVTLDMVMCTASILNLCALSIDRY 133

QY 120 LLIAHPKLPQVFSAGKIVLALVSTWVVGVSFAPLWPIYILVPVCTCSFDRIRGRPYT 179
Db 134 TAVAMPMLYNTRYSSKRRVTVMIS--IVWVLSFT-----ISCPLLFGLNNADQNE 181

QY 180 TILMGIYFVLGLSSVGIF-----YCLIHQ-----VKRAAQAAL----- 212
Db 182 CIIANPAFVYSSIVSFYVPIVTLVLLVIKIYIVLRRRKRKRVNKRSSRAFRAPLX 241

QY 213 -----DQYKLRQASIHNS-----HVARTDEAMPGRFQELD-SRLASGGPSEGISSEPV 260
Db 242 GNCTHPEDMKLCTVIMKNSGSPFVNRVDAAR--RAQELEMEMLSSTSPPTRYSPIP 299

QY 261 AATTQTLEGDSSEVG-----DQINSKRAKQMAEKSPPEASAKAQPIKGA 304
Db 300 PSHHQLTLPDPSHHGLHSTPDSAPKEKNGHAKDHPKIAKIFEIQTMPNGKTRTS-LKTM 358

QY 305 RRAPDSSSEFGKVTRMCFVLCFALSYPFLLNILDARVQAPRVVHMLAANLTW--- 361
Db 359 SRRKLSQQKEKATQMLAIVLGVFIICWLPPFFITHILNIHCDI-NIPPVLYSAFTWLGIV 417

QY 362 NGCINPVLVYAAMNRQFRQAYGSIL 385
Db 418 NSAVNPIIYTTFNIEFRKAPLKIL 441

RESULT 3

US-08-333-977-18

; Sequence 18, Application US/08333977

; Patent No. 5594108

; GENERAL INFORMATION:

; APPLICANT: Van Tol, Hubert H.M.

; APPLICANT: Civelii, Olivier

; TITLE OF INVENTION: A No. 5594108e1 Human Dopamine Receptor and Uses

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Allegretti & Witcoff, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/333,977

; FILING DATE: 03-NOV-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/626,618

; FILING DATE: 7 DEC 1990

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5594108nan, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 90,1092

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

; TELEX: 810-221-8317

```
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-333-977-18

Query Match          14.4%; Score 293; DB 1; Length 443;
Best Local Similarity 25.9%; Pred. No. 2.8e-18;
Matches 115; Conservative 66; Mismatches 179; Indels 84; Gaps 16;

QY      2 WNSSDANFSCYHESVLGYRYVAVSWGVAVTGTVGNVLTLLALAIQPKLRTFRNLLIAN 61
Db      22 FNGSDGKADRPH-----YHYVATLLTLLIAVI-VFQNVLCMAVSREKALQTTNYLIVS 75

QY      62 LTLADLLYCTLLQPFSDTYLHL--HWRTGATFCRVFGLLLFASNSVSLTCLIALGRY 119
Db      76 LAVADLLVATLMPVWV--YLEVVGEWKFSRIHCDIFVTLDMVMCTASINLCAISIDRY 133

QY      120 LLIAHPKLFPOVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVVCCTCFDRIRGRPYT 179
Db      134 TAVAMPMLYNTYSSKRVTVNIS--IVWVLSFT-----ISCPLLFGLNNADQNE 181

QY      180 TILMGIYFVLGLSSVGIF-----YCLIHQ-----VKRAAQAL----- 212
Db      182 CIIANPAFVYSSIVSFYPPFIVTLVYIKIYIVLRRRRKRVNTRSSRAFRAPLPLK 241

QY      213 -----DQYKLRQASIHNS-----HVARTDEAMPGRFQELD-SRLASGGSESGISSEPV 260
Db      242 GNCTHPEDMKLCTVIMKNSGFPVNRVDAAR--RAQELEMEMLSSTSPERTRYSPIP 299

QY      261 AATTQTLGDSSEVG-----DQINSKRAKQMAEKSPPEASAKAQPIKGA 304
Db      300 PSHHQLTLPDPSHHGLSTPDSAPKPKNGHAKDHPKIAKIFEIQTMPNGKTRTS-LKTM 358

QY      305 RRAPDSSSEFGKVTMCFVFLCFALSYPFLLLNLILDARVQAPRVVHMLAANLTWL--- 361
Db      359 SRRLKSQKKEKATQMLAIVLGVFIICWLPFFITHILNIHDC-NIPPVLYSAFTWLGIV 417

QY      362 NGCINPVLYAAMNRQFRQAYGSIL 385
Db      418 NSAVNPIIYTTFNIEFRKAPLKIL 441

RESULT 4
US-08-194-338-3
; Sequence 3, Application US/08194338
; Patent No. 5474898
; GENERAL INFORMATION:
; APPLICANT: Venter, John C.
; APPLICANT: Fraser, Claire M.
; APPLICANT: McCombie, William R.
; TITLE OF INVENTION: OCTOPAMINE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,338
; FILING DATE: 08-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 07/676,174
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH101.001DV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-194-338-3

Query Match          14.3%; Score 291.5; DB 1; Length 515;
Best Local Similarity 25.4%; Pred. No. 4.6e-18;
Matches 104; Conservative 73; Mismatches 162; Indels 71; Gaps 14;

QY      2 WNS-SDANFSCYHE---SVLGYRYV--AVSWGVVVA---VTGTGVNVLTLALAIQPKL 51
Db      17 WGEIKDANFTGPNQTSNSTLPLQDVTTRAISVGLVGLGAFILFAIVGNILVILSVACNRHL 76

QY      52 RTRENLLIANLTADLLYCTLLQPFSDTYLHLHWRTGATFCRVFGLLLFASNSVSLTIL 111
Db      77 RTPTNYFIVNLAIDLLTSFTVLPFSATIEVLGYWVWVLSVVISIGPLLGWK---EPAPNDD 192

QY      112 CLIALGRYLLIAHPKLFPOVFSAGKIVLALVSTWVVG-VASFAPL--WPIYILVPVVCCTC 168
Db      137 CAISIDRYIGVRYSLQYPTLVTRKAILALLSVWVLSVVISIGPLLGWK---EPAPNDD 192

QY      169 SFDRIKGRPYTTILMGI-YFVLGLSSVGIFYCLIHQVKRAAQALDQYKLRQASIHSHV 227
Db      193 KECGVTEEPFYALFSSLSGYFIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMS----- 246

QY      228 ARTDEAMPGRFQELDRLASGSPSEGISSEPVSAATTQTLGDSSEVGDQINSKRAKQMA 287
Db      247 -----NSKELTLRIHKNPHE-----DTLSSTKAK--- 271

QY      288 EKSPPEASAKAQPIKGARRAPDSSESSEFGKVTMCFVFLCFALSYPFL---LNILDAR 344
Db      272 -GHNPRSSIAVKLFKFSRE-KKAATLGIIVGM-----FILCWLPFFIALPLGSLFST 322

QY      345 VQAPRVVHMLAANLTWLNCGINPVLYAAMNRQFRQAYGSILKRGPRRSFHR 394
Db      323 LKPPDAVEKVVWTLGYFNSCLNPILYPCSSKEFKRAFMRLGCGQCRSGRR 372

RESULT 5
US-09-688-415-10
; Sequence 10, Application US/09688415
; Patent No. 6448011
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A
; APPLICANT: Forray, Carlos
; APPLICANT: Weinshank, Richard L
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA 1 ADRENERGIC RECEPTORS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 41337aza
; CURRENT APPLICATION NUMBER: US/09/688,415
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/474,551
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 515
```

```
;
;
; TYPE: PRT
; ORGANISM: Hamster sp.
US-09-688-415-10
Query Match      14.2%; Score 290.5; DB 4; Length 515;
Best Local Similarity 25.1%; Pred. No. 5.7e-18;
Matches 103; Conservative 75; Mismatches 161; Indels 71; Gaps 14;

QY 2 WNS-SDANFSCYHE---SVLGYRYV--AVSWGVVVA---VTGTGNGVLTLLALAIQPKL 51
Db 17 WGEKLDANFTGPNQTSNSTLPQLDVTTRAISVGLVGFILFAIVGNILVILSVACNRHL 76
QY 52 RTFRNLLIANLTADLLYCTLLQPFSDVTYHLHWRGTGATFCRVFGLLLFASNSVSILT 111
Db 77 RTPNYFIVNLAIDLSTLFTVLPFSATLEVGLVWVLTGRIFCDIWAAVDVLCCTASILSL 136
QY 112 CLIALGRYLLIAHPKLPQVFSAGKIVLALVSTWVVG--VASFAPL--WPIYILVPVVCTC 168
Db 137 CAISIDRYIGVRSYLSQYPTLVTRRKAILALLSVWLSTVISIGPLLGWK----EPAPNDD 192
QY 169 SFDRIGRPYTTILMGI-YFVLGLSSVGIFYCLIHQRQVKRAAQALDQYKLRQASIHSHV 227
Db 193 KECGVTEEPFYALFSSLSGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMS-----246
QY 228 ARTDEAMPGRFQELDSRLASGSPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMA 287
Db 247 -----NSKELTLRIHSKNFHE-----DTLSSTKAK---271
QY 288 EKSPPEASAKAQPICKGARRAPDSSEFGKVTMCFVFLCFALSYPFLL---LNILDAR 344
Db 272 -GHNPRSSIAVKLFKFSRE-KKAAKTLGIVVGM-----FILCWLPFFIALPLGSLFST 322
QY 345 VQAPRVVHMLAANLTWNGCINPVLVYAMNRQFRQAYGSILKRGPRSFHR 394
Db 323 LKPPDAVKVFWLGYFNLSCLNPIIYPCSSKEFKRAFMRILGCQCRSGRR 372

RESULT 6
US-08-444-734A-7
; Sequence 7, Application US/08444734A
; Patent No. 5610282
; GENERAL INFORMATION:
; APPLICANT: Sibley, David R.
; APPLICANT: Monsma, Frederick J.
; APPLICANT: Mahan, Lawrence C.
; APPLICANT: McVittie, Loris D.
; TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
; TITLE OF INVENTION: receptor linked to adenylyl cyclase activation and
; TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
; TITLE OF INVENTION: cell lines
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,734A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,917
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/548,714
; FILING DATE: 06-JUL-1990
```

```
;
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: NIH065.001FW1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-444-734A-7

Query Match      14.1%; Score 288.5; DB 1; Length 515;
Best Local Similarity 25.1%; Pred. No. 8.6e-18;
Matches 103; Conservative 74; Mismatches 162; Indels 71; Gaps 14;

QY 2 WNS-SDANFSCYHE---SVLGYRYV--AVSWGVVVA---VTGTGNGVLTLLALAIQPKL 51
Db 17 WGEKLDANFTGPNQTSNSTLPQLDVTTRAISVGLVGFILFAIVGNILVILSVACNRHL 76
QY 52 RTFRNLLIANLTADLLYCTLLQPFSDVTYHLHWRGTGATFCRVFGLLLFASNSVSILT 111
Db 77 RTPNYFIVNLAIDLSTLFTVLPFSATLEVGLVWVLTGRIFCDIWAAVDVLCCTASILSL 136
QY 112 CLIALGRYLLIAHPKLPQVFSAGKIVLALVSTWVVG--VASFAPL--WPIYILVPVVCTC 168
Db 137 CAISIDRYIGVRSYLSQYPTLVTRRKAILALLSVWLSTVISIGPLLGWK----EPAPNDD 192
QY 169 SFDRIGRPYTTILMGI-YFVLGLSSVGIFYCLIHQRQVKRAAQALDQYKLRQASIHSHV 227
Db 193 KECGVTEEPFYALFSSLSGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMS-----246
QY 228 ARTDEAMPGRFQELDSRLASGSPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMA 287
Db 247 -----NSKELTLRIHSKNFHE-----DTLSSTKAK---271
QY 288 EKSPPEASAKAQPICKGARRAPDSSEFGKVTMCFVFLCFALSYPFLL---LNILDAR 344
Db 272 -GHNPRSSIAVKLFKFSRE-KKAAKTLGIVVGM-----FILCWLPFFIALPLGSLFST 322
QY 345 VQAPRVVHMLAANLTWNGCINPVLVYAMNRQFRQAYGSILKRGPRSFHR 394
Db 323 LKPPDAVKVFWLGYFNLSCLNPIIYPCSSKEFKRAFMRILGCQCRSGRR 372

RESULT 7
US-08-406-855A-22
; Sequence 22, Application US/08406855A
; Patent No. 5861309
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30
```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,855A
; FILING DATE: 21-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-406-855A-22

Query Match 14.1%; Score 288.5; DB 2; Length 515;
Best Local Similarity 25.1%; Pred. No. 8.6e-18;
Matches 103; Conservative 74; Mismatches 162; Indels 71; Gaps 14;

QY 2 WNS-SDANFSCYHE----SVLGRYV--AVSWGVVVA---VTGTGNVLTLLALAIQPKL 51
Db 17 WGEKLDANFTGPNQTSNSTLPQLDVTTRAISVGLVGAFILFAIVGNILVILSVACNRHL 76
QY 52 RTRENFLLIANLTADLLYCTLLQPFSDVDTYLHLHWRTGATFCRVFGLLFPASNSVSILTL 111
Db 77 RTPNTYFIVNLAIAADLLSFTVLPFSATLEVLGYVWVLSVVISIGPLLGWK----EPAPNDD 136
QY 112 CLIALGRYLLIAHPKLFPPQVFSAGKIVLALVSTWVVG--VASFAPL--WPIYILVPVWCTC 168
Db 137 CAISIDRYIGVRYSLQYPTLVTRRKAILALLSVVLSVVISIGPLLGWK----EPAPNDD 192
QY 169 SFDRIRGRPYTTILMGI-YFVLGLSSVGIFYCLIHQVKRAAQALDQYKLRQASIHNSHV 227
Db 193 KECGVTEEPFYALFSSLSGFIPLAVILMYCRVYIVAKRTTKNLEAGVMKEMS-----246
QY 228 ARTDEAMPGRFQELDSRLASGSPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMA 287
Db 247 -----NSKELTLRIHKNFHE-----DTLSSTKAK---271
QY 288 EKSPPEASAKAQPICKGARRAPDSSESEFGKVTMCFVFLCFALSYPFLL---LNILDAR 344
Db 272 -GHNPRSSIAVKLFKFSRE-KKAAKTLGIVVGM-----FILCWLPFFIALPLGSLFST 322
QY 345 VQAPRVVHMLAANLTWLNCGINPVLVYAAAMNQFRQAYGSILKRGPRSFHR 394
Db 323 LKPPDAVFKVFWLGYFNFSCLNPIIYPCSSKEFKRAFMRIILGCQCRSGRR 372

RESULT 8
US-09-206-899-22
; Sequence 22, Application US/09206899
; Patent No. 6083705
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,899
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,855
; FILING DATE: 21-AUG-1995.
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-206-899-22

Query Match 14.1%; Score 288.5; DB 3; Length 515;
Best Local Similarity 25.1%; Pred. No. 8.6e-18;
Matches 103; Conservative 74; Mismatches 162; Indels 71; Gaps 14;

QY 2 WNS-SDANFSCYHE----SVLGRYV--AVSWGVVVA---VTGTGNVLTLLALAIQPKL 51
Db 17 WGEKLDANFTGPNQTSNSTLPQLDVTTRAISVGLVGAFILFAIVGNILVILSVACNRHL 76
QY 52 RTRENFLLIANLTADLLYCTLLQPFSDVDTYLHLHWRTGATFCRVFGLLFPASNSVSILTL 111
Db 77 RTPNTYFIVNLAIAADLLSFTVLPFSATLEVLGYVWVLSVVISIGPLLGWK----EPAPNDD 136
QY 112 CLIALGRYLLIAHPKLFPPQVFSAGKIVLALVSTWVVG--VASFAPL--WPIYILVPVWCTC 168
Db 137 CAISIDRYIGVRYSLQYPTLVTRRKAILALLSVVLSVVISIGPLLGWK----EPAPNDD 192
QY 169 SFDRIRGRPYTTILMGI-YFVLGLSSVGIFYCLIHQVKRAAQALDQYKLRQASIHNSHV 227
Db 193 KECGVTEEPFYALFSSLSGFIPLAVILMYCRVYIVAKRTTKNLEAGVMKEMS-----246
QY 228 ARTDEAMPGRFQELDSRLASGSPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMA 287
Db 247 -----NSKELTLRIHKNFHE-----DTLSSTKAK---271
QY 288 EKSPPEASAKAQPICKGARRAPDSSESEFGKVTMCFVFLCFALSYPFLL---LNILDAR 344
Db 272 -GHNPRSSIAVKLFKFSRE-KKAAKTLGIVVGM-----FILCWLPFFIALPLGSLFST 322
QY 345 VQAPRVVHMLAANLTWLNCGINPVLVYAAAMNQFRQAYGSILKRGPRSFHR 394
Db 323 LKPPDAVFKVFWLGYFNFSCLNPIIYPCSSKEFKRAFMRIILGCQCRSGRR 372

RESULT 9
US-09-688-415-9
; Sequence 9, Application US/09688415
; Patent No. 6448011
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A
; APPLICANT: Forray, Carlos
; APPLICANT: Weinsank, Richard L
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA 1 ADRENERGIC RECEPTORS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 41337aza
; CURRENT APPLICATION NUMBER: US/09/688,415
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/474,551
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 23


```

; SOFTWARE: PatentIn Ver. 2.1.1
; SEQ ID NO 9
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-688-415-9

```

Query Match	14.1%;	Score	287.5;	DB 4;	Length	515;			
Best Local Similarity	24.9%;	Pred. No.	1.1e-17;						
Matches	96;	Conservative	71;	Mismatches	151;	Indels	67;	Gaps	12;

RESULT 10
US-08-722-001-25
; Sequence 25, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHALC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.

[illegible]

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```


; Sequence 4, Application US/08334698
; Patent No. 5556753
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,698
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/952,798
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 376901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-334-698-4

Query Match 14.0%; Score 285.5; DB 1; Length 520;
Best Local Similarity 24.8%; Pred. No. 1.6e-17;
Matches 96; Conservative 71; Mismatches 151; Indels 69; Gaps 12;

Qy 23 AVSWGCVVVA---VTGTGCVNLTLLALAIQPKLRTRENLIIANLTADLLCYCTLLQPFSD 79
Db 45 AISVGLVLGAFILFAIVGNILVILSVACNRHLRTPNTNYFIVNLAMADLLLSFTVLPFSAA 104

Qy 80 TYLHLHWRTGATFCRVFGLLLFASNSVILTCLIALGRYLLIAHPKLPQVPSAKGIVL 139
Db 105 LEVLGYWVLGRIFCDIWAADVLCCTASILSLCAISIDRYIGVYSLQYPTLVTRRKAIL 164

Qy 140 ALVSTWVVG-VASFAPL--WPIYILVPVVTCTSFDRIRGRPYTTILMGI-YFVLGLSSVG 195
Db 165 ALLSVWVLSTVISIGPLLGWK----EPAPNDKCEGVTEEPFYALFSLGSPYIPLAVIL 220

Qy 196 IFYCLTHRQVKRAAQALDOYKLRQASIHNSHVARTDEAMGRFOELDSRLASGGPSEGIS 255
Db 221 VMYCRVYIVAKRTTKNLEAGVNMKMS-----NSKELTLRIHSKNFHE--- 262

Qy 256 SEPVSAAATTQLEGDSSEVGQINSKRAQMAEKSPPEASAKAQPIKGARRAPDSSEFG 315
Db 263 -----DTLSSTKAK----GHNPRSSIAVKLFKFSRE-KKAAKTLG 297

Qy 316 KYTRMCFVFLCFALSYPFL--LNILDARVQAPRVVHMLAANLTWLNGINPVLVYAA 372
Db 298 IVVGM-----FILCWLPFFIALPLGSLFSTLTKPPDAVFKVFWLGYFNSCLNPIIYPC 350

Qy 373 MNRQFRQAYGSIL-----KRGPFSFHR 394
Db 351 SSKEFKRAFVRILGCCQCRGRGRRRRR 377

Search completed: September 24, 2004, 08:40:54
Job time : 31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:25:34 ; Search time 103.224 Seconds
(without alignments)
7048.158 Million cell updates/sec

Title: US-10-029-436-1

Perfect score: 1311

Sequence: 1 ttgaatgctagggtctgtatt.....caggaccagtgccaggta 1311

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1256.4	95.8	1498	2	US-08-775-428-1	Sequence 1, Appli
2	87.8	6.7	1382	4	US-09-364-425B-22	Sequence 22, Appli
3	87.8	6.7	1584	1	US-08-748-485-2	Sequence 2, Appli
4	87.8	6.7	1584	4	US-09-016-434-284	Sequence 284, App
5	87	6.6	2481	1	US-08-467-568-1	Sequence 1, Appli
6	87	6.6	2481	2	US-09-030-582-1	Sequence 1, Appli
7	87	6.6	2481	5	PCT-US94-09051-1	Sequence 1, Appli
8	83	6.3	921	1	US-08-722-001-17	Sequence 17, Appli
9	83	6.3	1567	1	US-08-722-001-24	Sequence 24, Appli
10	83	6.3	1738	1	US-08-334-698-3	Sequence 3, Appli
11	83	6.3	1738	1	US-08-228-932-3	Sequence 3, Appli
12	83	6.3	1738	1	US-08-468-939-3	Sequence 3, Appli
13	83	6.3	1738	2	US-08-406-855A-3	Sequence 3, Appli
14	83	6.3	1738	2	US-08-722-190-3	Sequence 3, Appli
15	83	6.3	1738	3	US-08-244-354-3	Sequence 3, Appli
16	83	6.3	1738	3	US-09-206-899-3	Sequence 3, Appli
17	83	6.3	1738	4	US-09-444-783-3	Sequence 3, Appli
18	83	6.3	1738	4	US-09-688-415-3	Sequence 3, Appli
19	83	6.3	1738	4	US-09-016-434-1402	Sequence 1402, Ap
20	83	6.3	1738	4	US-09-444-783-3	Sequence 3, Appli
21	83	6.3	1738	5	PCT-US95-04203-3	Sequence 3, Appli
22	80	6.1	1092	3	US-09-077-675A-15	Sequence 15, Appli
23	80	6.1	1092	4	US-09-077-674-15	Sequence 15, Appli
24	80	6.1	3129	3	US-09-077-675A-14	Sequence 14, Appli
25	80	6.1	3129	4	US-09-077-674-14	Sequence 14, Appli
26	78.4	6.0	1095	4	US-09-743-475-2	Sequence 2, Appli
27	78.4	6.0	4009	4	US-09-743-475-1	Sequence 1, Appli

28	75	5.7	1088	3	US-09-077-675A-6	Sequence 6, Appli
29	75	5.7	1088	4	US-09-077-674-6	Sequence 6, Appli
30	75	5.7	1101	4	US-09-016-434-1148	Sequence 1148, Ap
31	75	5.7	1101	4	US-09-170-496D-87	Sequence 87, Appli
32	75	5.7	1101	4	US-09-170-496D-209	Sequence 209, App
33	75	5.7	1101	4	US-09-364-425B-44	Sequence 44, Appli
34	75	5.7	1122	3	US-09-077-675A-9	Sequence 9, Appli
35	75	5.7	1122	4	US-09-077-674-9	Sequence 9, Appli
36	73.6	5.6	1050	4	US-09-762-661A-1	Sequence 1, Appli
37	70.2	5.4	7218	1	US-08-232-463-14	Sequence 14, Appli
38	70	5.3	1080	3	US-08-875-540-14	Sequence 14, Appli
39	70	5.3	1080	4	US-09-473-634-14	Sequence 14, Appli
40	69.8	5.3	1601	1	US-08-722-001-7	Sequence 7, Appli
41	69.8	5.3	1639	1	US-08-334-698-5	Sequence 5, Appli
42	69.8	5.3	1639	1	US-08-228-932-5	Sequence 5, Appli
43	69.8	5.3	1639	1	US-08-468-939-5	Sequence 5, Appli
44	69.8	5.3	1639	2	US-08-406-855A-5	Sequence 5, Appli
45	69.8	5.3	1639	2	US-08-722-190-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-775-428-1
; Sequence 1, Application US/08775428
; Patent No. 5976834
; GENERAL INFORMATION:
; APPLICANT: Sathe, Ganesh
; APPLICANT: Fuetterer, Wendy
; APPLICANT: Bergsma, Derx
; APPLICANT: Ellis, Catherine
; TITLE OF INVENTION: CDNA CLONE HNFJD15 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,428
; FILING DATE: 09-JAN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4060
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1498 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-775-428-1

Query Match 95.8%; Score 1256.4; DB 2; Length 1498;
Best Local Similarity 99.9%; Pred. No. 0;

RESULT 3

US-08-748-485-2
 ; Sequence 2, Application US/08748485
 ; Patent No. 5817480
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Murry, Lynn E.
 ; TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/748,485
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0159 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1584 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: Consensus
 ; CLONE: 1722180
 US-08-748-485-2

Query Match 6.7%; Score 87.8; DB 1; Length 1584;
 Best Local Similarity 53.7%; Pred. No. 1.3e-15;
 Matches 182; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY	160	GGCACCCTGGGCAATGTGCTCACCCTACTGGCCCTTGGCCATCCAGCCCAAGCTCCGTACC	219
Db	287	GTCTGCTGGGAAACCTGGTCACCTTGTACAAGATCCTACTCCTCCTCACC	346
QY	220	CGATTCAACCTGCTCATAGCCAACTCAGCTGATCTCCTCTACTGCACGCTCCTT	279
Db	347	CTCAGCAACAAGTTCGTCTTCCAACTTCTGCTGCTGCTGCTGCTGCTGCTG	406
QY	280	CAGCCCTTCTGTGGACACCTACCTCCACCTGCGACCGGTGCCACCTTCTGC	339
Db	407	CTGCTCTTGTGGTACGAGCTCCATCCGAGGAAATGGATCTTTGGTGTAGTGGTGC	466
QY	340	AGGGTATTTGGGCTCCTCTTTTGGCTCCAAATCTGTCTCCATCCTGACCTTCTGC	399
Db	467	AACCTTCTCTGCTCCTCTACTACCTGCTGATCAGCTCTGCCAGCATGCTAACCTTCGGGTC	526
QY	400	ATCGCACTGGACGCTACCTCCTCAATGGCCCACTTCTTTTCCCAAGTTTTCAGT	459
Db	527	ATTGCCATCGACCGCTACTATGCTGCTCTGTACCCCATGGTGTACCCCATGAAGATCACA	586

QY 460 GCGAAGGGGATAGTGTGGCACTGGTGAGCACCCTGGGTT 498
 Db 587 GCGAAGGGGCTGTGATGGCACTTGTCTACATCTGGCTT 625

RESULT 4
 US-09-016-434-284
 ; Sequence 284, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 284:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1584 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: BLADNOT06
 ; CLONE: 1722180
 US-09-016-434-284

Query Match 6.7%; Score 87.8; DB 4; Length 1584;
 Best Local Similarity 53.7%; Pred. No. 1.3e-15;
 Matches 182; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY	160	GGCACCCTGGGCAATGTGCTCACCCTACTGGCCCTTGGCCATCCAGCCCAAGCTCCGTACC	219
Db	287	GTCTGCTGGGAAACCTGGTCACCTGTCACCTTGTACAAGATCCTACTCCTCACC	346
QY	220	CGATTCAACCTGCTCATAGCCAACTCAGCTGATCTCCTCTACTGCACGCTCCTT	279
Db	347	CTCAGCAACAAGTTCGTCTTCCAACTTCTGCTGCTGCTGCTGCTGCTGCTG	406
QY	280	CAGCCCTTCTGTGGACACCTACCTCCACCTGCGACCTGGCGCACCGGTGCCACCTTCTGC	339
Db	407	CTGCTCTTGTGGTACGAGCTCCATCCGAGGAAATGGATCTTTGGTGTAGTGGTGC	466
QY	340	AGGGTATTTGGGCTCCTCTTTTGGCTCCAAATCTGTCTCCATCCTGACCTTCTGCCTC	399
Db	467	AACCTTCTCTGCTCCTCTACTACCTGCTGATCAGCTCTGCCAGCATGCTAACCTTCGGGTC	526

QY	400	ATCGCACTGGGACGCTACCTCCTCATTTGCCCCACCCTAAGCTTTTTCCCCAAGTTTTTCAGT	459
Dδ	527	ATTGCCATCGACCGCTACTATGCTGTCTGTACCCCATGGTGTAACCCATGAAGATCAC	586
QY	460	GCCAAAGGGGATAGTGTGGCACTGGTGAGCACCTGGGTT	498
Dδ	587	GGGAACCGGGCTGTGATGGCACTTGTCATCATCTGGCTT	625

```

RESULT 5
US-08-467-568-1
; Sequence 1, Application US/08467568
; Patent No. 5817477
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL R
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,568
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-324
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2481 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101..1687
; US-08-467-568-1

```

	Query Match	6.6%;	Score 87;	DB 1;	Length 2481;
	Best Local Similarity	53.7%;	Pred. No. 2.8e-15;		
	Matches 180;	Conservative 0;	Mismatches 155;	Indels 0;	Gaps 0;
QY	164	CCGTGGGCAATGTGTCACCCCTACTGGCCCTTGGCCCATCCAGCCCAAGCTCCGTACCCGAT	223		
Db	225	CCTGGGAAACCTGGTCATCGTGGTCACCTTGTAACAAGATCCTACCTCCTCACCCCTCA	284		
QY	224	TCAACCTGCTCATAGCCAAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGC	283		
Db	285	GCAACAAGTTCGTCTTCAGCCTGACTCTGTCCAACTTCCTGCTGTCCTGGTGTGGTGTGC	344		
QY	284	CCTTCTCTGIGBACACCTACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGCAGGG	343		
Db	345	CTTTTGTGGTGACGAGCTCCATCCGACGGGAATGGATCTTTGGTGTAGTGTGGTGCAACT	404		
QY	344	TATTTGGGCTCCTCCTTTTGGCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCG	403		
Db	405	TCTCTGCCCTCCTCTACCTGTCTGATCAGCTCTGCCAGCATGCTTAACCTCGGGGTCAATG	464		

[illegible]

```

RESULT 6
US-09-030-582-1
; Sequence 1, Application US/09030582
; Patent No. 5994506
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL R
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,582
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/467,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-324
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2481 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101..1687
;
US-09-030-582-1

```

	Query Match	6.6%;	Score 87;	DB 2;	Length 2481;
	Best Local Similarity	53.7%;	Pred. No. 2.8e-15;		
	Matches 180;	Conservative	0;	Mismatches 155;	Indels 0; Gaps 0;
QY	164	CCGTGGGCAATGTGCTCACCCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGAT	223		
Db	225	CCTGGGAACCTGGTCATCGTGGTCACCTTGTAACAAGATCCTACCTCCTCACCCCTCA	284		
QY	224	TCAACCTGCTCATAGCCAACTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGC	283		
Ddb	285	GCAACAAGTTCGTCTTCAGCCCTGACTCTGTGTCCAACTTCCTGTGTCCGTGTTGGTGTGC	344		
QY	284	CCTTCTCTGTGGACACCTACTCCACTGCACCTGGCGCACCGGTGCCACCTTCTGCAGGG	343		
Ddb	345	CTTTTGTGTGACGAGCTCCATCCGACGGGAATGGATCTTTGGTGTAGTGTGGTGCACCT	404		

QY 344 TATTGGGCTCCTCTCTTTTGGCCCTCCAAATTCGTCTCCATCCTGACCCCTCTGCCTCATCG 403
Db 405 TCTCTGCCCTCCTCTACCTGCTGATCAGCTCTGCCAGCATGCTAACCCCTCGGGGTCATTG 464
QY 404 CACTGGGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCA 463
Db 465 CCATCGACCGCTACTATGCTGTCTGTACCCCATGGTGTACCCCATGAAGATCACAGGGA 524
QY 464 AGGGGATAGTGTGGCACTGGTGAGCACCTGGGTT 498
Db 525 ACCGGGCTGTGATGGCACTTGTCTACATCTGGCTT 559

RESULT 7

PCT-US94-09051-1
; Sequence 1, Application PC/TUS9409051
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Adrenergic Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09051
; FILING DATE: Submitted herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2481 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
PCT-US94-09051-1

Query Match 6.6%; Score 87; DB 5; Length 2481;
Best Local Similarity 53.7%; Pred. No. 2.8e-15;
Matches 180; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 164 CCGTGGGCAATGTGCTCACCCCTACTGGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGAT 223
Db 225 CCTGGGAAACCTGGTCATCGTGGTCACCTTGTAACAAGAAGTCTACCTCCTCACCCCTCA 284
QY 224 TCAACCTGCTCATAGCAACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGC 283
Db 285 GCAACAAGTTCGCTTTCAGCCTGACTCTGTCCAACTTCCTGCTGTCGCTGTTGGTGCTGC 344
QY 284 CCTTCTCTGTGACACCTACCTCCACCTGCACTGGCGCACCGTGCCACCTTCTGCGAGG 343
Db 345 CTTTTGTGTGACGAGCTCCATCCGACGGAATGGATCTTTTGTGTAGTGTGTTGCTACT 404
QY 344 TATTGGGCTCCTCCTCTTTTGGCCCTCCAAATTCGTCTCCATCCTGACCCCTCTGCCTCATCG 403

Db 405 TCTCTGCCCTCCTCTACCTGCTGATCAGCTCTGCCAGCATGCTAACCCCTCGGGTCAATTG 464
QY 404 CACTGGGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCA 463
Db 465 CCATCGACCGCTACTATGCTGTCTGTACCCCATGGTGTACCCCATGAAGATCACAGGGA 524
QY 464 AGGGGATAGTGTGGCACTGGTGAGCACCTGGGTT 498
Db 525 ACCGGGCTGTGATGGCACTTGTCTACATCTGGCTT 559

RESULT 8

US-08-722-001-17
; Sequence 17, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHALC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19169Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-722-001-17

Query Match 6.3%; Score 83; DB 1; Length 921;
Best Local Similarity 52.1%; Pred. No. 2.5e-14;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 160 GGCACCGTGGCAATGTGCTCACCCCTACTGGGCTTGGCCATCCAGCCCAAGCTCCGTACC 219
Db 183 GCCATCGTGGCAACATCCTAGTCATCTTGTGTGGCCTGCAACCGGCACCTGCGGACG 242
QY 220 CGATTCAACCTGCTCATAGCCAACTCACACTGGCTGATCTCCTCTACTGACGCTCCTT 279
Db 243 CCCACCAACTACTTCATTGTTCACCTGGCCATGGCCGACCTGCTGTGTGAGCTTACCCGTC 302

US-08-334-698-3

Query Match	6.3%;	Score 83;	DB 1;	Length 1738;
Best Local Similarity	52.1%;	Pred. No. 3.5e-14;		
Matches 185;	Conservative 0;	Mismatches 170;	Indels 0;	Gaps 0;
QY	160	GGCACCGTGGCAATGTGCTCACCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACC	219	
Db	298	GCCATCGTGGCAACATCCTAGTCATCTTGTCTGTGGCCTGCAACCGGCACCTGGCGACG	357	
QY	220	CGATTCAACCTGCTCATFAGCAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTT	279	
Db	358	CCCACCAACTACTTCAATTGTCAACCTGGCCATGGCCGACCTGCTGTTGAGCTTCAACCGTC	417	
QY	280	CAGCCCTTCTCTGTGGACACCTTACCTCCACCTGCACCTGGGCACCGGTGCCACCTTCTGC	339	
Db	418	CTGCCCTTCTCAGCGGCCCTAGAGGTGCTCGGCTACTGGGTGCTGGGCGGATCTTCTGT	477	
QY	340	AGGGTATTTGGGCTCCTCCTTTTGGCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCCTC	399	
Db	478	GACATCTGGGCGACCCGTGGATGTCTGTGCTGCACAGCGTCCATCTGAGCCTGTGGCGCC	537	
QY	400	ATCGCACTGGGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTTCCTCCAAAGTTTTCAGT	459	
Db	538	ATCTCCATCGATCGCTACATCGGGGTGGCTACTCTCTGCAGTATCCCAACGCTGGTCACC	597	
QY	460	GCCAAGGGGATAGTGTGGCACTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCT	514	
Db	598	CGGAGGAAGGCCATCTTGGCGTGTCTCAGTGTCTGGGTCTTGTCCACCGTCATCT	652	

RESULT 11

US-08-228-932-3
; Sequence 3, Application US/08228932
; Patent No. 5578611
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
; APPLICANT: Theresa A. Brancheck, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
; TITLE OF INVENTION: PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,932
; FILING DATE: 13-APR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N

TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-722-190-3

Query Match 6.3%; Score 83; DB 2; Length 1738;
Best Local Similarity 52.1%; Pred. No. 3.5e-14;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 160 GGCACCGTGGCAATGTGCTCACCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACC 219
Db 298 GCCATCGTGGCAACATCTAGTCATCTGTGTGGCCTGCAACCGGACCTGGGACG 357

QY 220 CGATTCAACCTGCTCATAGCCAACTCACACTGGCTGATCTCTACTGACGCTCCTT 279
Db 358 CCCACCACTACTTCACTGTCAACCTGGCCATGGCCGACCTGTTGAGCTTCACCGTC 417

QY 280 CAGCCCTTCTGTGGACACCTACCTCCACCTGCACCTGGCCACCGGTGCCACCTTCTGC 339
Db 418 CTGCCCTTCTCAGCGGCCCTAGAGGTGCTCGGCTACTGGGTGCTGGGCGGATCTTCTGT 477

QY 340 AGGTATTGGGCTCCTCCTTTTGGCTCCCAATTCGTCTCCATCCTGACCCCTCTGCCTC 399
Db 478 GACATCTGGCAGCCGTGGATGCTCTGTGCTGCACAGCGTCCATCTGAGCCTGTGGCC 537

QY 400 ATGGCACTGGGACGCTACCTCCTCATTTGGCCACCTGAGTGGGCTGGGCGTGGCCAGCT 514
Db 538 ATCTCCATCGATCGCTACATCGGGGTGCGTACTCTCTGAGTATCCACCGTGTCACT 597

QY 460 GCCAAGGGATAGTGTGGCACTGGTGAGCACTGGGTGTGGGCGTGGCCAGCT 514
Db 598 CGGAGGAAGGCCATCTTGGCGCTGCTCAGTGTCTGGGTCTTGTCACCGTCACT 652

RESULT 15
US-08-244-354-3
Sequence 3, Application US/08244354
Patent No. 6015819
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, et al.
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TREAT BENIGN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,354
FILING DATE: April 1, 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-D-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-244-354-3

Query Match 6.3%; Score 83; DB 3; Length 1738;
Best Local Similarity 52.1%; Pred. No. 3.5e-14;
Matches 185; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 160 GGCACCGTGGCAATGTGCTCACCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACC 219
Db 298 GCCATCGTGGCAACATCTAGTCATCTGTGTGGCCTGCAACCGGACCTGGGACG 357

QY 220 CGATTCAACCTGCTCATAGCCAACTCACACTGGCTGATCTCTACTGACGCTCCTT 279
Db 358 CCCACCACTACTTCACTGTCAACCTGGCCATGGCCGACCTGTTGAGCTTCACCGTC 417

QY 280 CAGCCCTTCTGTGGACACCTACCTCCACCTGCACCTGGCCACCGGTGCCACCTTCTGC 339
Db 418 CTGCCCTTCTCAGCGGCCCTAGAGGTGCTCGGCTACTGGGTGCTGGGCGGATCTTCTGT 477

QY 340 AGGTATTGGGCTCCTCCTTTTGGCTCCCAATTCGTCTCCATCCTGACCCCTCTGCCTC 399
Db 478 GACATCTGGCAGCCGTGGATGCTCTGTGCTGCACAGCGTCCATCTGAGCCTGTGGCC 537

QY 400 ATGGCACTGGGACGCTACCTCCTCATTTGGCCACCTGAGTGGGCTGGGCGTGGCCAGT 459
Db 538 ATCTCCATCGATCGCTACATCGGGGTGCGTACTCTCTGAGTATCCACCGTGTCACT 597

QY 460 GCCAAGGGATAGTGTGGCACTGGTGAGCACTGGGTGTGGGCGTGGCCAGCT 514
Db 598 CGGAGGAAGGCCATCTTGGCGCTGCTCAGTGTCTGGGTCTTGTCACCGTCACT 652

Search completed: September 24, 2004, 04:51:46
Job time : 105.224 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:04:24 ; Search time 5339.89 Seconds
(without alignments)
10641.181 Million cell updates/sec

Title: US-10-029-436-1
Perfect score: 1311
Sequence: 1 ttgaatgctaggtttctgatt.....caggaccacaaagtggcaggta 1311

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:
29: em_vi:
30: em_htg_hum:
31: em_htg_inv:
32: em_htg_other:
33: em_htg_mus:
34: em_htg_pln:
35: em_htg_rod:
36: em_htg_mam:
37: em_htg_vrt:
38: em_sy:
39: em_htgo_hum:
40: em_htgo_mus:
41: em_htgo_other:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1306	99.6	141003	9	AC078778	AC078778 Homo sapi
2	1256.4	95.8	1493	9	AF237762	AF237762 Homo sapi
3	1256.4	95.8	1498	6	AR083245	AR083245 Sequence
4	1256.4	95.8	1535	9	BC020614	BC020614 Homo sapi
5	1256.4	95.8	1546	6	AX549299	AX549299 Sequence
6	1256.4	95.8	1546	9	AF282693	AF282693 Homo sapi
7	1256.4	95.8	1595	6	AX247564	AX247564 Sequence
8	1191	90.8	1191	6	BD144298	BD144298 Novel G-p
9	1191	90.8	1191	9	AB083586	AB083586 Homo sapi
10	901	68.7	207421	2	AC021643	AC021643 Mus muscu
11	897	68.4	1574	10	BC023249	BC023249 Mus muscu
12	895.8	68.3	1611	10	AF272948	AF272948 Rattus no
13	891	68.0	244845	2	AC126846	AC126846 Homo sapi
14	754	57.5	141003	2	AC016463	AC016463 Homo sapi
15	87.8	6.7	1382	6	BD229108	BD229108 Endogeneo
16	87.8	6.7	1382	6	AR431783	AR431783 Sequence
17	87.8	6.7	1382	6	AX549134	AX549134 Sequence
18	87.8	6.7	1382	9	AF091890	AF091890 Homo sapi
19	87.8	6.7	1584	6	AR044154	AR044154 Sequence
20	87.8	6.7	1584	6	AR269721	AR269721 Sequence
21	87.8	6.7	1584	6	BD007520	BD007520 Novel his
22	87.8	6.7	1590	9	AY275468	AY275468 Homo sapi
23	87.8	6.7	2400	9	AK122656	AK122656 Homo sapi
24	87.8	6.7	2733	9	BC028163	BC028163 Homo sapi
25	87	6.6	2481	6	AR044088	AR044088 Sequence
26	87	6.6	2481	6	AR091709	AR091709 Sequence
27	87	6.6	2481	6	AX573819	AX573819 Sequence
28	87	6.6	2481	6	BD144779	BD144779 Adrenergi
29	86.2	6.6	1663	6	AX467017	AX467017 Sequence
30	83	6.3	1560	9	HUMAIAR	L31773 Human alpha
31	83	6.3	1738	6	AR030766	AR030766 Sequence
32	83	6.3	1738	6	AR088757	AR088757 Sequence
33	83	6.3	1738	6	AR101770	AR101770 Sequence
34	83	6.3	1738	6	I26009	I26009 Sequence 3
35	83	6.3	1738	6	I30002	I30002 Sequence 3
36	83	6.3	1738	6	I83625	I83625 Sequence 3
37	83	6.3	1738	6	AR228241	AR228241 Sequence
38	83	6.3	1738	6	AR270839	AR270839 Sequence
39	83	6.3	1738	6	AR373863	AR373863 Sequence
40	83	6.3	1738	6	AX136023	AX136023 Sequence
41	83	6.3	1738	6	AX137520	AX137520 Sequence
42	83	6.3	1738	9	HSU03865	U03865 Human adren
43	83	6.3	1786	6	AX548750	AX548750 Sequence
44	83	6.3	2669	9	HUMADRENA	M99589 Homo sapien
45	83	6.3	8727	9	AC127458	AC127458 Homo sapi

ALIGNMENTS

RESULT 1
AC078778
LOCUS
DEFINITION
AC078778 Homo sapiens 12 BAC RP11-968A15 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
AC078778
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AC078778 141003 bp DNA linear PRI 21-FEB-2003
Homo sapiens 12 BAC RP11-968A15 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
AC078778 GI:23307958
HTG.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 141003)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,

Pred. No. is the number of results predicted by chance to have a

Barbaria, J., Benton, J., Bimane, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstein, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 141003)
Worley, K.C.
Direct Submission
Submitted (03-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 141003)
Worley, K.C.
Direct Submission
Submitted (27-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 141003)
Worley, K.C.
Direct Submission
Submitted (25-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 141003)
Worley, K.C.
Direct Submission
Submitted (21-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 25, 2002 this sequence version replaced gi:22477001.
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of

the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

FEATURES	Source	Location/Qualifiers
misc_feature		1. 141003 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="12" /clone="RP11-968A15" complement(1..2005) /note="overlaps bases 1..2005 of clone AC079313" /function="clone overlap"
STS		460..659 /standard_name="RH158"
STS		18075..18234 /standard_name="NIB1371"
STS		18111..18242 /standard_name="A002C47"
STS		18229..18400 /standard_name="RH78595"
STS		18349..18457 /standard_name="D12S1927"
STS		19062..19158 /standard_name="Bdya3g12"
STS		71395..71512 /standard_name="D11S2560"
STS		77459..77710 /standard_name="WI-7866"
STS		77500..77704 /standard_name="RH44735"
STS		84170..84320 /standard_name="D12S1994"
STS		84697..84944 /standard_name="SHGC-2501"
STS		96032..96157 /standard_name="RH93620"
misc_feature		124640..124653 /function="single clone coverage"
STS		128073..128188 /standard_name="D12S1966"
STS		128451..128635 /standard_name="RH102227"
STS		129604..129730 /standard_name="SGC34021"

/protein_id="AAK01857.1"
/db_xref="GI:127111471"
/translation="MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTVGNVLTLLA
LAIQKLRTRFNLLIANLADLLYCTLLQPFSDVTYHLHWRCTFCRVFGLLLFA
NSVSILTLCLIALGRYLLIAHPKLPQVFSAGKIVLALVSTWVGVAFAFLWPIYI
LVPVCTCSFDRIRGRPYITILMGIYFVLGLSSVGFYCLIHQVKRAAQALDQYKLR
QASIHNVARTDEAMPGRFQELDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGD
QINSKAKQMAEKSPPEASAKAOPIKGARRAPDSSSFQKVTIRMCFVFLCPALSYP
FLLNLILDARVQAPRVVHMLAANLTWLNCGINPVLVYAMNRQFRQAYGSILKRGPRSF
HRLH"

ORIGIN

Query Match 95.8%; Score 1256.4; DB 9; Length 1493;
Best Local Similarity 99.9%; Pred. No. 4.2e-313;
Matches 1257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 TTAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG 108
Db 57 TCAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG 116

QY 109 CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGGCTGTGACAGGCACCGTG 168
Db 117 CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGGCTGTGACAGGCACCGTG 176

QY 169 GGCAATGTGTCACCCCTACTGGCCTTGGCCATCCAGCCCAAGTCCGTACCCGATTCAAC 228
Db 177 GGCAATGTGTCACCCCTACTGGCCTTGGCCATCCAGCCCAAGTCCGTACCCGATTCAAC 236

QY 229 CTGCTCATAGCCAACTCAGACTGGCTGATCTCCTACTGACGCTCCTTCAGCCCTTC 288
Db 237 CTGCTCATAGCCAACTCAGACTGGCTGATCTCCTACTGACGCTCCTTCAGCCCTTC 296

QY 289 TCTGTGGACACCTACCTCCACCTGCACTGGCGGCACCGGTGCAACCTTCTGACGGTATTT 348
Db 297 TCTGTGGACACCTACCTCCACCTGCACTGGCGGCACCGGTGCAACCTTCTGACGGTATTT 356

QY 349 GGGCTCCTCCTTTTGCCTCCAAATCTGTCTCCATCCTGACCTCTGCCTCATCGCACTG 408
Db 357 GGGCTCCTCCTTTTGCCTCCAAATCTGTCTCCATCCTGACCTCTGCCTCATCGCACTG 416

QY 409 GGACGCTACTCCTCATTTGCCCAACCTTAAGCTTTTTCGCCAAGTTTTCAGTGCCAAAGGG 468
Db 417 GGACGCTACTCCTCATTTGCCCAACCTTAAGCTTTTTCGCCAAGTTTTCAGTGCCAAAGGG 476

QY 469 ATAGTGTGGCACTGGTGAGCACCTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTGG 528
Db 477 ATAGTGTGGCACTGGTGAGCACCTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTGG 536

QY 529 CCTATTATATCCTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCCGG 588
Db 537 CCTATTATATCCTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCCGG 596

QY 589 CCTTACACCACTCCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATC 648
Db 597 CCTTACACCACTCCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATC 656

QY 649 TTCTATTGCCTCATCCACCGCAGGTCAACAGCAGCAGCAGGCACTGGACCAATACAAG 708
Db 657 TTCTATTGCCTCATCCACCGCAGGTCAACAGCAGCAGGCACTGGACCAATACAAG 716

QY 709 TTGGCAGGCAAGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT 768
Db 717 TTGGCAGGCAAGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT 776

QY 769 CGTTTCCAGGAGCTGGACAGAGGTTAGCATCAGGAGGACCCAGTGAGGGATTTTCATCT 828
Db 777 CGTTTCCAGGAGCTGGACAGAGGTTAGCATCAGGAGGACCCAGTGAGGGATTTTCATCT 836

QY 829 GAGCAGTCAGTGTGCCACACCCAGACCCCTGGAGGGGACTCATCAGAAGTGGGAGAC 888
Db 837 GAGCAGTCAGTGTGCCACACCCAGACCCCTGGAGGGGACTCATCAGAAGTGGGAGAC 896

QY 889 CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCC 948

Db 897 CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCC 956

QY 949 AAAGCCCAGCCAAATTAAGGAGGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAG 1008

Db 957 AAAGCCCAGCCAAATTAAGGAGGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAG 1016

QY 1009 GTGACTCGAATGCTTTTGTGCTGTGTTCCCTCTGCTTTTGGCCCTGAGCTACATCCCTTCTTG 1068

Db 1017 GTGACTCGAATGCTTTTGTGCTGTGTTCCCTCTGCTTTTGGCCCTGAGCTACATCCCTTCTTG 1076

QY 1069 CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCCGGGTGGTCCACATGCTTGTGCC 1128

Db 1077 CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCCGGGTGGTCCACATGCTTGTGCC 1136

QY 1129 AACCTCACCTGGCTCAATGGTTGCATCAACCCCTGTGCTCTATGACGCCATGAACCCCAA 1188

Db 1137 AACCTCACCTGGCTCAATGGTTGCATCAACCCCTGTGCTCTATGACGCCATGAACCCCAA 1196

QY 1189 TTCCGCCAAGCATATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT 1248

Db 1197 TTCCGCCAAGCATATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT 1256

QY 1249 TAGAACTGTGACCCTAGTCAACCAAGATTCAGGACTGTCTCTCCAGGACCAAAAGTGGC 1306

Db 1257 TAGAACTGTGACCCTAGTCAACCAAGATTCAGGACTGTCTCTCCAGGACCAAAAGTGGC 1314

RESULT 3

AR083245
LOCUS AR083245 1498 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 1 from patent US 5976834.
ACCESSION AR083245
VERSION AR083245.1 GI:10010035
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1498)
AUTHORS Sathre,G.Madhusudan., Fueterer,W.S., Bergsma,D.John. and Ellis,C.
TITLE cDNA clone HNFJD15 that encodes a novel human 7-transmembrane receptor
JOURNAL Patent: US 5976834-A 1 02-NOV-1999;
FEATURES Location/Qualifiers
source 1..1498
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 95.8%; Score 1256.4; DB 6; Length 1498;
Best Local Similarity 99.9%; Pred. No. 4.2e-313;
Matches 1257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 TTAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG 108

Db 64 TCAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG 123

QY 109 CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGTGTGACAGGCACCGTG 168

Db 124 CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGTGTGACAGGCACCGTG 183

QY 169 GGCAATGTGCTCACCCCTACTGGCCTTGGCCATCCAGCCCAAGTCCGTACCCGATTCAAC 228

Db 184 GGCAATGTGCTCACCCCTACTGGCCTTGGCCATCCAGCCCAAGTCCGTACCCGATTCAAC 243

QY 229 CTGCTCATAGCCAACTCAGACTGGCTGATCTCCTTACTGCAAGCTCCTTCAGCCCTTC 288

Db 244 CTGCTCATAGCCAACTCAGACTGGCTGATCTCCTTACTGCAAGCTCCTTCAGCCCTTC 303

QY 289 TCTGTGGACACCTACCTCCACCTGCAGTGGCGGACCGGTGCCACCTTCTGCAGGGTATTT 348

Db 304 TCTGTGGACACCTACCTCCACCTGCAGTGGCGGACCGGTGCCACCTTCTGCAGGGTATTT 363

QY	349	GGGCTCCTCCTTTTGGCTCCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTG	408
Db	364	GGGCTCCTCCTTTTGGCTCCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTG	423
QY	409	GGACGTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGG	468
Db	424	GGACGTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGG	483
QY	469	ATAGTGTGGCACTGGTGAGCACCTGGGTTCTGGGCGTGGCCAGCTTTGCTCCCTCTGG	528
Db	484	ATAGTGTGGCACTGGTGAGCACCTGGGTTCTGGGCGTGGCCAGCTTTGCTCCCTCTGG	543
QY	529	CCTATTATATCCTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGGCCGG	588
Db	544	CCTATTATATCCTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGGCCGG	603
QY	589	CCTTACACCACTCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATC	648
Db	604	CCTTACACCACTCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATC	663
QY	649	TTCTATTGCCTCATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAG	708
Db	664	TTCTATTGCCTCATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAG	723
QY	709	TTGCGACAGGCAAGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGT	768
Db	724	TTGCGACAGGCAAGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGT	783
QY	769	CGTTTCAGGAGCTGGACAGCAGGTTAGCTAGCATCAGGAGACCCAGTGAGGGGATTTCATCT	828
Db	784	CGTTTCAGGAGCTGGACAGCAGGTTAGCTAGCATCAGGAGACCCAGTGAGGGGATTTCATCT	843
QY	829	GAGCCAGTCAGTGTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGAC	888
Db	844	GAGCCAGTCAGTGTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGAC	903
QY	889	CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCC	948
Db	904	CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCC	963
QY	949	AAAGCCAGCCCAATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAG	1008
Db	964	AAAGCCAGCCCAATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAG	1023
QY	1009	GTGACTCGAATGTGTTTGTGCTGTCTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTG	1068
Db	1024	GTGACTCGAATGTGTTTGTGCTGTCTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTG	1083
QY	1069	CTGCTCAACATTCTGGATGCCAGAGTCCAGGCTCCCCGGGTGGTCCACATGCTTGTGCC	1128
Db	1084	CTGCTCAACATTCTGGATGCCAGAGTCCAGGCTCCCCGGGTGGTCCACATGCTTGTGCC	1143
QY	1129	AACCTCACTGGCTCAATGTTTGCAATCAACCCCTGTGCTCTATGTCAGCCATGAACCGCAA	1188
Db	1144	AACCTCACTGGCTCAATGTTTGCAATCAACCCCTGTGCTCTATGTCAGCCATGAACCGCAA	1203
QY	1189	TTCCGCCAAGCATATGGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCAT	1248
Db	1204	TTCCGCCAAGCATATGGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCAT	1263
QY	1249	TAGAAGTGTGACCCCTAGTCAACCAAGATTCAGGACTGTCTCTCCAGGACCAAGTGCC	1306
Db	1264	TAGAAGTGTGACCCCTAGTCAACCAAGATTCAGGACTGTCTCTCCAGGACCAAGTGCC	1321
RESULT 4			
BC020614			
LOCUS			
DEFINITION			
Homo sapiens G protein-coupled receptor 84, mRNA (cDNA clone			
MGC:22224 IMAGE:4279185), complete cds.			
ACCESSION			
BC020614			
VERSION			
BC020614.1 GI:18089044			
KEYWORDS			
MGC.			

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1535)
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 1535)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 35 Row: k Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9966838.
source	Location/Qualifiers 1..1535 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:22224 IMAGE:4279185" /tissue type="Brain, primitive neuroectodermal" /clone_lib="NIH_MGC_56" /lab_host="DH10B" /note="Vector: pDNR-LIB" 1..1535 /gene="GPR84" /note="synonyms: EX33, GPCR4" /db_xref="LocusID:53831" /db_xref="MIM:606383" 101..1291 /codon_start=1 /product="inflammation-related G protein-coupled receptor EX33" /protein_id="AAH20614.1"
gene	
CDS	

/db_xref="GI:18089045"
/db_xref="LocusID:53831"
/translation="MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTVGNVLTLLA
LAIQPKLRFRNLLIANLTLADLLYCTLLQPFSDTYLHLHWRGTGATFRVGLLLFA
SNSVILTLCLIALGRLIAHPKLPQVFSAGTIVLALVSTWVGVAFPALWPIYI
LVPVCTCSFDRIRGRPYTILMGIFYVLGLSSVGFYCLIHROVKRAQAALDQYKLR
QASIHSHVARTDEAMPGRFOELDSRLASGGPSGEGISSEPVSAATTOTLEGDSEVGD
QINSKRAQMAEKSPPEASAKAOPIKGARRAPDSSEBFGKVRMCFVFLCFALSYP
FILLNILDARVQAPRVVHMLAANLTWLNCGINPVLVYAMNRQFRQAYGSILKRGPRSF
HRLH"
misc_feature 323..742
/note="7tm_1; Region: 7 transmembrane receptor (rhodopsin
family)"
/db_xref="CDD:pfam00001"
misc_feature 1010..1210
/note="7tm_1; Region: 7 transmembrane receptor (rhodopsin
family)"
/db_xref="CDD:pfam00001"
ORIGIN
Query Match 95.8%; Score 1256.4; DB 9; Length 1535;
Best Local Similarity 99.9%; Pred. No. 4.2e-313;
Matches 1257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 49 TTAGCCTCTATCATGTGGAACAGCTCTGACGCCAACCTTCTCCTGCTACCATGAGTCTGTG 108
Db 89 TCAGCCTCTATCATGTGGAACAGCTCTGACGCCAACCTTCTCCTGCTACCATGAGTCTGTG 148
QY 109 CTGGGCTATCGTTATGTTGCAAGTTAGCTGGGGGGTGGTGGCTGTGACAGGACCCGTG 168
Db 149 CTGGGCTATCGTTATGTTGCAAGTTAGCTGGGGGGTGGTGGCTGTGACAGGACCCGTG 208
QY 169 GGCAATGTCTCACCCTACTGGCCTTGGCCCATCCAGCCCAAGCTCCGTACCCGATTAAC 228
Db 209 GGCAATGTCTCACCCTACTGGCCTTGGCCCATCCAGCCCAAGCTCCGTACCCGATTAAC 268
QY 229 CTGCTATAGCCAACTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC 288
Db 269 CTGCTATAGCCAACTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC 328
QY 289 TCTGTGACACCTACCTCCACCTGCACTGGCGCACCGGTGGCCACCTTCTGCAGGATATT 348
Db 329 TCTGTGACACCTACCTCCACCTGCACTGGCGCACCGGTGGCCACCTTCTGCAGGATATT 388
QY 349 GGGCTCCTCTCTTTTGCCTCCCAATCTGTCTCCATCCTGACCCCTCTGCCCTCATCGCACTG 408
Db 389 GGGCTCCTCTCTTTTGCCTCCCAATCTGTCTCCATCCTGACCCCTCTGCCCTCATCGCACTG 448
QY 409 GGACGCTACCTCCTCATTTGCCCAACCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGG 468
Db 449 GGACGCTACCTCCTCATTTGCCCAACCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGG 508
QY 469 ATAGTGCTGGCACTGGTGAGCACCTGGGTTGTGGCGGTGGCCAGCTTTGCTCCCTCTGG 528
Db 509 ATAGTGCTGGCACTGGTGAGCACCTGGGTTGTGGCGGTGGCCAGCTTTGCTCCCTCTGG 568
QY 529 CCTATTATATCCTGGTACCTGTAGTCTGCACCTGCACTTTGACCGCATCCGAGGCCCGG 588
Db 569 CCTATTATATCCTGGTACCTGTAGTCTGCACCTGCACTTTGACCGCATCCGAGGCCCGG 628
QY 589 CCTTACACCACCATCCTCATATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATC 648
Db 629 CCTTACACCACCATCCTCATATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATC 688
QY 649 TTCTATTCCTCATCCACCGCCAGGTCAAACGAGCAGCAGCAGGCACTGGACCAATACAAG 708
Db 689 TTCTATTCCTCATCCACCGCCAGGTCAAACGAGCAGCAGCAGGCACTGGACCAATACAAG 748
QY 709 TTGCGACAGGCAAGCATCCACCTCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT 768
Db 749 TTGCGACAGGCAAGCATCCACCTCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT 808
QY 769 CGTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGAGGCCAGCCAGTGAGGGGATTTTCATCT 828

Db 809 CGTTTCCAGGAGCTGGACAGCAGGTAGCATCAGGAGGCCAGTGGGGATTTTCATCT 868
QY 829 GAGCCAGTCAGTGTCTGCCACCACCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGAC 888
Db 869 GAGCCAGTCAGTGTCTGCCACCACCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGAC 928
QY 889 CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCC 948
Db 929 CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCC 988
QY 949 AAAGCCACGCCAATTAAAGGAGGCCAGAGCTCCGGATTCTTCATCGGAATTTGGGAAG 1008
Db 989 AAAGCCACGCCAATTAAAGGAGGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAG 1048
QY 1009 GTGACTCGAATGTGTTTTGCTGTGTCTCTCTGCTTTTGGCCCTGAGCTACATCCCTTCTTG 1068
Db 1049 GTGACTCGAATGTGTTTTGCTGTGTCTCTCTGCTTTTGGCCCTGAGCTACATCCCTTCTTG 1108
QY 1069 CTGCTCAACATTTCTGGATGCCAGATCCAGGCTCCCGGGTGGTCCACATGCTTGTCTGCC 1128
Db 1109 CTGCTCAACATTTCTGGATGCCAGATCCAGGCTCCCGGGTGGTCCACATGCTTGTCTGCC 1168
QY 1129 AACCTACCTGGCTCAATGGTTGCATCAACCCCTGTGCTCTATGCAGCCATGAACCGCAA 1188
Db 1169 AACCTACCTGGCTCAATGGTTGCATCAACCCCTGTGCTCTATGCAGCCATGAACCGCAA 1228
QY 1189 TTCCGCCAAGCATATGGCTCCATTTTAAAGAGGGGCCCGGAGTTTCCATAGGCTCCAT 1248
Db 1229 TTCCGCCAAGCATATGGCTCCATTTTAAAGAGGGGCCCGGAGTTTCCATAGGCTCCAT 1288
QY 1249 TAGAACTGTGACCTTAGTCACCAAGATTTCAGGACTGTCTCCTCCAGGACCAAGTGGC 1306
Db 1289 TAGAACTGTGACCTTAGTCACCAAGATTTCAGGACTGTCTCCTCCAGGACCAAGTGGC 1346
RESULT 5
AX549299
LOCUS AX549299 1546 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 584 from Patent WO02061087.
ACCESSION AX549299
VERSION AX549299.1 GI:25813960
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 584 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES Location/Qualifiers
source 1..1546
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 95.8%; Score 1256.4; DB 6; Length 1546;
Best Local Similarity 99.9%; Pred. No. 4.2e-313;
Matches 1257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 49 TTAGCCTCTATCATGTGGAACAGCTCTGACGCCAACCTTCTCCTGCTACCATGAGTCTGTG 108
Db 79 TCAGCCTCTATCATGTGGAACAGCTCTGACGCCAACCTTCTCCTGCTACCATGAGTCTGTG 138
QY 109 CTGGGCTATCGTTATGTTGCAAGTTAGCTGGGGGTGGTGGCTGTGACAGGACCCGTG 168
Db 139 CTGGGCTATCGTTATGTTGCAAGTTAGCTGGGGGTGGTGGCTGTGACAGGACCCGTG 198

QY 169 GGCAATGTGCTCACCCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAAC 228
Db 199 GGCAATGTGCTCACCCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAAC 258
QY 229 CTGCTCATAGCCAAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC 288
Db 259 CTGCTCATAGCCAAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC 318
QY 289 TCTGTGACACACTACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGATATT 348
Db 319 TCTGTGACACACTACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGATATT 378
QY 349 GGGCTCCTCCTTTTGGCTCCTCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTG 408
Db 379 GGGCTCCTCCTTTTGGCTCCTCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTG 438
QY 409 GGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGG 468
Db 439 GGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGG 498
QY 469 ATAGTGTGGCACTGGTGAGCACTGGTGTGGCGGTGGCCAGCTTTTGCTCCCTCTGG 528
Db 499 ATAGTGTGGCACTGGTGAGCACTGGTGTGGCGGTGGCCAGCTTTTGCTCCCTCTGG 558
QY 529 CCTATTATATCCTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCGG 588
Db 559 CCTATTATATCCTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCGG 618
QY 589 CCTTACACCAACCATCCTCATGGGCATCTACTTTGTGCTTGGCTCAGCAGTGTGGCATC 648
Db 619 CCTTACACCAACCATCCTCATGGGCATCTACTTTGTGCTTGGCTCAGCAGTGTGGCATC 678
QY 649 TTCTATTGCCCTCATCCACCGCCAGGTCAAACGAGCAGCAGGCACCTGGACCAATACAAG 708
Db 679 TTCTATTGCCCTCATCCACCGCCAGGTCAAACGAGCAGCAGGCACCTGGACCAATACAAG 738
QY 709 TTGCGACAGGCAAGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGTGT 768
Db 739 TTGCGACAGGCAAGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGTGT 798
QY 769 CGTTTCAGGAGCTGGACAGCAGGTAGCATCAGGAGGACCCAGTCAGGGGATTTCATCT 828
Db 799 CGTTTCAGGAGCTGGACAGCAGGTAGCATCAGGAGGACCCAGTCAGGGGATTTCATCT 858
QY 829 GAGCCAGTCAGTGTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGAC 888
Db 859 GAGCCAGTCAGTGTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGAC 918
QY 889 CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCC 948
Db 919 CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCC 978
QY 949 AAAGCCAGCCCAATTAAAGGAGCCAGAAGACTCCGGATTCTTCATCGGAATTTGGGAAG 1008
Db 979 AAAGCCAGCCCAATTAAAGGAGCCAGAAGACTCCGGATTCTTCATCGGAATTTGGGAAG 1038
QY 1009 GTGACTCGAATGTGTTTGTGCTGTCTCTGCTTTGGCCCTGAGCTACATCCCTCTCTTG 1068
Db 1039 GTGACTCGAATGTGTTTGTGCTGTCTCTGCTTTGGCCCTGAGCTACATCCCTCTCTTG 1098
QY 1069 CTGCTCAACATTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTCC 1128
Db 1099 CTGCTCAACATTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTCC 1158
QY 1129 AACCTCACCTGGCTCAATGGTTGCATCAACCCCTGTGCTCTATGCGCCCATGAACCGCCAA 1188
Db 1159 AACCTCACCTGGCTCAATGGTTGCATCAACCCCTGTGCTCTATGCGCCCATGAACCGCCAA 1218
QY 1189 TTCCGCCAAGCATATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT 1248
Db 1219 TTCCGCCAAGCATATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT 1278
QY 1249 TAGAACTGTGACCCTAGTCAACCAGAAATTAGGACTGTCTCTCTCCAGGACCAAGTGGC 1306

Db 1279 TAGAACTGTGACCCTAGTCAACCAGAAATTCAGGACTGTCTCTCTCCAGGACCAAGTGGC 1336
RESULT 6
AF282693 1546 bp mRNA linear PRI 23-SEP-2002
LOCUS Homo sapiens inflammation-related G protein-coupled receptor EX33
DEFINITION (EX33) mRNA, complete cds.
ACCESSION AF282693
VERSION AF282693.1 GI:96522260
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1546)
AUTHORS Yousefi,S., Cooper,P.R., Potter,S.L., Mueck,B. and Jarai,G.
TITLE Cloning and expression analysis of a novel G-protein-coupled
receptor selectively expressed on granulocytes
J. Leukoc. Biol. 69 (6), 1045-1052 (2001)
MEDLINE 21297471
PUBMED 11404393
REFERENCE 2 (bases 1 to 1546)
AUTHORS Yousefi,S., Cooper,P., Mueck,B., Potter,S. and Jarai,G.
TITLE Direct Submision
JOURNAL Submitted (26-JUN-2000) NHRC, Wimbleshurst, Horsham, West Sussex
RH12 5AB, UK
FEATURES
Location/Qualifiers
1..1546
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..1546
/gene="EX33"
91..1281
/gene="EX33"
/codon_start=1
/product="inflammation-related G protein-coupled receptor
EX33"
/protein_id="AAF91467.1"
/db_xref="GI:96522261"
/translation="MWNSSDANFSCYHESVLGYRYVAVSWGVVAVTGTGTVGNVLTLLA
LAIQPKLRTRFNLLIANLTADLLYCTLLQPFSDTVLHLHWRGTGATFCRVFGLLLFA
SNSVILTLCLIALGRYLLIAHPKLFQVFSAGKIVLALVSTWVGVASFAFLWPIYI
LVPVCTCSFDRIGRPYTILMGIYFVLGSSVGFYCLIHQVKRAAQALDQYKLR
QASIHNVARTDEAMPGRFQELDSRLASGSPGSEFVSAATTQTLEGDSSEVGD
QINSKRAQMAEKSPPEASAKAQPIKGARRAPDSSSEFGKVTMCFVFLCFALSYP
FLILNILDARVQAPRVVHMLAANLTWNGCINPVLAAAMNRQFRQAYGSILKRGPRSF
HRLH"

ORIGIN

Query Match 95.8%; Score 1256.4; DB 9; Length 1546;
Best Local Similarity 99.9%; Pred. No. 4.2e-313;
Matches 1257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 49 TTAGCCTCTATCATGTGGAACAGCTCTGACGCCCAACTTCTCCTGCTACCATGAGTCTGTG 108
Db 79 TCAGCCTCTATCATGTGGAACAGCTCTGACGCCCAACTTCTCCTGCTACCATGAGTCTGTG 138
QY 109 CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGCACCGTG 168
Db 139 CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGCACCGTG 198
QY 169 GGCAATGTGCTCACCCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCCGATTCAAC 228
Db 199 GGCAATGTGCTCACCCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCCGATTCAAC 258
QY 229 CTGCTCATAGCCAAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC 288
Db 259 CTGCTCATAGCCAAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC 318
QY 289 TCTGTGGACACCTACCTCCACCTGCACCTGGCGGACCGGTGCCACCTTCTGCAGGGTATTT 348


```
QY 829 GAGCCAGTCAGTGTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGAC 888
Db 908 GAGCCAGTCAGTGTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGAC 967
QY 889 CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCC 948
Db 968 CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCC 1027
QY 949 AAAGCCAGCCCAATTAAGGAGGAGCAGAGAGCTCCGGATCTTTCATCGGAATTTGGGAAG 1008
Db 1028 AAAGCCAGCCCAATTAAGGAGGAGCAGAGAGCTCCGGATCTTTCATCGGAATTTGGGAAG 1087
QY 1009 GTGACTCGAATGTGTTTGTGCTGTGTTTCTCTGCTTTTGCCTGAGCTACATCCCTTCTTG 1068
Db 1088 GTGACTCGAATGTGTTTGTGCTGTGTTTCTCTGCTTTTGCCTGAGCTACATCCCTTCTTG 1147
QY 1069 CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCCGGGTGGTCCACATGCTTGTGCC 1128
Db 1148 CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCCGGGTGGTCCACATGCTTGTGCC 1207
QY 1129 AACCTCACCTGGCTCAATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAACGCCAA 1188
Db 1208 AACCTCACCTGGCTCAATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAACGCCAA 1267
QY 1189 TTCCGCCAAGCATATGGCTCAATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT 1248
Db 1268 TTCCGCCAAGCATATGGCTCAATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT 1327
QY 1249 TAGAACTGTGACCCCTAGTCACAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1306
Db 1328 TAGAACTGTGACCCCTAGTCACAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1385

RESULT 8
BD144298
LOCUS BD144298 1191 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel G-protein coupled receptors.
ACCESSION BD144298
VERSION BD144298.1 GI:27850056
KEYWORDS JP 2002112793-A/23.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1191)
AUTHORS Haga,T., Takeda,S. and Miyake,N.
TITLE Novel G-protein coupled receptors
JOURNAL Patent: JP 2002112793-A 23 16-APR-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002112793-A/23
PD 16-APR-2002
PF 09-FEB-2001 JP 2001034434
PI TATSUYA HAGA,SHIGEKI TAKEDA,NARIKI MIYAKE
PC C12N15/09,A01K67/027,A61K38/00,A61K39/395,A61K39/395,A61K45/00, PC
A61K48/00,
PC A61P43/00,C07K14/705,C07K16/28,C07K19/00,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
G01N33/566//
PC C12P21/08,C12N15/00,A61K37/02,C12N5/00
CC Novel G-protein coupled receptors
FH Key Location/Qualifiers
FT CDS (1)..(1191).
FEATURES
source
1..1191
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
```

Query Match 90.8%; Score 1191; DB 6; Length 1191;

ORIGIN

```
Best Local Similarity 100.0%; Pred. No. 2.5e-296;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 ATGTGGAAACAGCTCTGACGGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 120
Db 1 ATGTGGAAACAGCTCTGACGGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 60
QY 121 TATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGACCGTGGGCAATGTGCTC 180
Db 61 TATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGACCGTGGGCAATGTGCTC 120
QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAAGCTCCGTAACCGATTCACCTGCTCATAGCC 240
Db 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAAGCTCCGTAACCGATTCACCTGCTCATAGCC 180
QY 241 AACCTCACACTGGCTGATCTCCTTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 300
Db 181 AACCTCACACTGGCTGATCTCCTTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 240
QY 301 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGTATTTGGGCTCCTCCTT 360
Db 241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGTATTTGGGCTCCTCCTT 300
QY 361 TTTGCTCCCAATTTCTCTCCATCTGACCCCTCTGCTCATCGCACTGGACGCTACCTC 420
Db 301 TTTGCTCCCAATTTCTCTCCATCTGACCCCTCTGCTCATCGCACTGGACGCTACCTC 360
QY 421 CTCATTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGSCA 480
Db 361 CTCATTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGSCA 420
QY 481 CTGGTGAGCAACCTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 540
Db 421 CTGGTGAGCAACCTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 480
QY 541 CTGGTACCTGTAGTCTGCACCTGCACTTTGACCGCATCCGAGGCGGCTTACACCAACC 600
Db 481 CTGGTACCTGTAGTCTGCACCTGCACTTTGACCGCATCCGAGGCGGCTTACACCAACC 540
QY 601 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCCTC 660
Db 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCCTC 600
QY 661 ATCCACCGCCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 720
Db 601 ATCCACCGCCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 660
QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTGTTCCAGGAG 780
Db 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTGTTCCAGGAG 720
QY 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCACT 840
Db 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCACT 780
QY 841 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 900
Db 781 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCCAGCCA 960
Db 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCCAGCCA 900
QY 961 ATTAAGGAGCCAGAAAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
Db 901 ATTAAGGAGCCAGAAAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
QY 1021 TGTTTTGTGTTTCTCTGCTTTTGCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1080
Db 961 TGTTTTGTGTTTCTCTGCTTTTGCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCAACCTCACCTGG 1140
```


Db 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGTCACCACTCACCTTG 1080
QY 1141 CTCAATGGTTGCATCAACCCCTGTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1200
Db 1081 CTCAATGGTTGCATCAACCCCTGTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1140
QY 1201 TATGGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1251
Db 1141 TATGGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191

RESULT 9
AB083586
LOCUS 1191 bp DNA linear PRI 24-MAY-2002
DEFINITION Homo sapiens GPCR gene for putative G-protein coupled receptor,
complete CDS, clone:hGPCR4.
ACCESSION AB083586
VERSION AB083586.1 GI:20152235
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
Takeda,S., Kadowaki,S., Haga,T., Takaesu,H. and Mitaku,S.
AUTHORS Identification of G protein-coupled receptor genes from the human
TITLE genome sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1191)
Takeda,S., Kadowaki,S., Haga,T., Takaesu,H. and Mitaku,S.
AUTHORS Direct Submission
TITLE Submitted (10-APR-2002) Shigeki Takeda, Gunma University,
JOURNAL Department of Biological and Chemical, Engineering, Faculty of
Department of Engineering; 1-5-1, Kiryu, Gunma 376-8515, Japan
(E-mail:stakeda@bce.gunma-u.ac.jp, Tel:+81-277-30-1434,
Fax:+81-277-30-1434)

FEATURES
source
1..1191
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="hGPCR4"
1..1191
/gene="GPCR"
1..1191
/gene="GPCR"
/note="predicted with SOSUI analysis"
/codon_start=1
/product="putative G-protein coupled receptor"
/protein_id="BAB89299.1"
/db_xref="GI:20152236"
/translation="MNSSDANFSCYHESVLGYRYVAVSVGVVAVTGVNVLTLA
LAIQKLRTRFNLLIANLTADLLYCTLLQPFSDTYLHLHRTGTGTCRVFGLLLFA
SNSVSLTLCLIALGRYLLIAHPKLPQVFSAGIVLALVSTWVGVASFAPLWPIYI
LVPVVTCSFDRIRGRPYTILMGIYFVLGLSSVIGIFYCLIHROVKRAAQALDQYKLR
QASIHNSHVARTDEAMPGRFOELDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGD
QINSKRAQMAEKSPPEASAKAOPKIGARRAPDSSEFSGKVTMCFVFLCFALSYP
FLLLNILDARVQAPRVVHMLAANLTWLNGLNPVLYAAMNRQFRQAYGSILKRGPRSF
HRLH"

ORIGIN
Query Match 90.8%; Score 1191; DB 9; Length 1191;
Best Local Similarity 100.0%; Pred. No. 2.5e-296;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 ATGTGGACAGCTCTGACGCCAATCTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 120
Db 1 ATGTGGACAGCTCTGACGCCAATCTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
QY 121 TATGTTGACGTTAGCTGGGGGGTGGTGGTGGTGTGACAGCACCGTGGGCAATGTGCTC 180
Db 61 TATGTTGACGTTAGCTGGGGGGTGGTGGTGGTGTGACAGCACCGTGGGCAATGTGCTC 120

QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
Db 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
QY 241 AACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACACC 300
Db 181 AACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACACC 240
QY 301 TACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGACAGGATTTTGGGCTCCTCCTT 360
Db 241 TACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGACAGGATTTTGGGCTCCTCCTT 300
QY 361 TTTGCTCCCAATTTCTGTCTCCATCTCTGACCTCTGCTCATCGCACTGGGACGTACCTC 420
Db 301 TTTGCTCCCAATTTCTGTCTCCATCTCTGACCTCTGCTCATCGCACTGGGACGTACCTC 360
QY 421 CTCATTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGGATAGTGTGGCA 480
Db 361 CTCATTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGGATAGTGTGGCA 420
QY 481 CTGGTGACACCTGGGTTGTGGCGTGGCCAGCTTTTGTCTCCCTCTGGCTATTATATC 540
Db 421 CTGGTGACACCTGGGTTGTGGCGTGGCCAGCTTTTGTCTCCCTCTGGCTATTATATC 480
QY 541 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGCCGGCTTACACCACC 600
Db 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGCCGGCTTACACCACC 540
QY 601 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTTGCTC 660
Db 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTTGCTC 600
QY 661 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 720
Db 601 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 660
QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCACTGCCTGGTCTTCCAGGAG 780
Db 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCACTGCCTGGTCTTCCAGGAG 720
QY 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT 840
Db 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT 780
QY 841 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 900
Db 781 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 960
Db 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
QY 961 ATTAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
Db 901 ATTAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
QY 1021 TGTTTTGCTGTGTTCTCTGCTTTTCCCTGAGCTACATCCCTCTTCTGTGCTCAACATT 1080
Db 961 TGTTTTGCTGTGTTCTCTGCTTTTCCCTGAGCTACATCCCTCTTCTGTGCTCAACATT 1020
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGTTGTGCCAACCTCACCTGG 1140
Db 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGTTGTGCCAACCTCACCTGG 1080
QY 1141 CTCAATGGTTGCATCAACCCCTGTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1200
Db 1081 CTCAATGGTTGCATCAACCCCTGTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1140
QY 1201 TATGGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1251
Db 1141 TATGGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191

RESULT 10
AC021643
LOCUS
DEFINITION
AC021643
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AC021643 207421 bp DNA linear HTG 15-MAY-2002
Mus musculus chromosome 15 clone RP23-169K7 strain C57BL6/J,
WORKING DRAFT SEQUENCE, 23 unordered pieces.
AC021643 GI:15143422
HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 207421)
Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R.,
Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A., Gordon,M.
and Kucherlapati,R.
High Throughput Mouse Sequencing
Unpublished
2 (bases 1 to 207421)
Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R.,
Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A., Gordon,M.
and Kucherlapati,R.
Direct Submission
Submitted (19-JAN-2000) Department of Molecular Genetics, Albert
Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
Bronx, NY 10461, USA
On Aug 9, 2001 this sequence version replaced gi:14717145.
-----Genome Center
Center: Harvard Partners Genome Center
Center Code: HPGC
Web site: <http://www.hpcgg.org/Sequence/mouse.html>
Contact: hpgc@medel.mgh.harvard.edu
-----Summary Statistics
Center project name: AAT
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 193187 at least Q20
*Consensus quality: 190826 at least Q30
*Consensus quality: 186718 at least Q40
Estimated insert size: agarose-FP - N/A
**Estimated insert size: 206981 - sum-of-contigs
Quality coverage: agarose-FP - N/A
Quality coverage: 6.5 x in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 38304: contig of 38304 bp in length
* 38305 38324: gap of unknown length
* 38325 68273: contig of 29949 bp in length
* 68274 68293: gap of unknown length
* 68294 89009: contig of 20716 bp in length
* 89010 89029: gap of unknown length
* 89030 108492: contig of 19463 bp in length
* 108493 108512: gap of unknown length
* 108513 120232: contig of 11720 bp in length
* 120233 120252: gap of unknown length
* 120253 131080: contig of 10828 bp in length
* 131081 131100: gap of unknown length
* 131101 142689: contig of 11589 bp in length
* 142690 142709: gap of unknown length
* 142710 155481: contig of 12772 bp in length
* 155482 155501: gap of unknown length
* 155502 164014: contig of 8513 bp in length
* 164015 164034: gap of unknown length
* 164035 171335: contig of 7301 bp in length
* 171336 171355: gap of unknown length
* 171356 179422: contig of 8067 bp in length

179423 179442: gap of unknown length
* 179443 185328: contig of 5886 bp in length
* 185329 185348: gap of unknown length
* 185349 190531: contig of 5183 bp in length
* 190532 190551: gap of unknown length
* 190552 196001: contig of 5450 bp in length
* 196002 196021: gap of unknown length
* 196022 200348: contig of 4327 bp in length
* 200349 200368: gap of unknown length
* 200369 202575: contig of 2207 bp in length
* 202576 202595: gap of unknown length
* 202596 203643: contig of 1048 bp in length
* 203644 203663: gap of unknown length
* 203664 204541: contig of 878 bp in length
* 204542 204561: gap of unknown length
* 204562 204816: contig of 255 bp in length
* 204817 204836: gap of unknown length
* 204837 204909: contig of 73 bp in length
* 204910 204929: gap of unknown length
* 204930 206958: contig of 2029 bp in length
* 206959 206978: gap of unknown length
* 206979 207177: contig of 199 bp in length
* 207178 207197: gap of unknown length
* 207198 207421: contig of 224 bp in length.
Location/Qualifiers
1. .207421
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL6/J"
/db_xref="taxon:10090"
/chromosome="15"
/clone="RP23-169K7"
/sex="male"
1. .38304
/note="assembly_name:Contig87"
38325. .68273
/note="assembly_name:Contig86"
68294. .89009
/note="assembly_name:Contig85"
89030. .108492
/note="assembly_name:Contig84"
108513. .120232
/note="assembly_name:Contig83"
120253. .131080
/note="assembly_name:Contig82"
131101. .142689
/note="assembly_name:Contig81"
142710. .155481
/note="assembly_name:Contig80"
155502. .164014
/note="assembly_name:Contig79"
164035. .171335
/note="assembly_name:Contig78"
clone end:SP6
vector_side:right"
171356. .179422
/note="assembly_name:Contig77"
179443. .185328
/note="assembly_name:Contig76"
185349. .190531
/note="assembly_name:Contig75"
190552. .196001
/note="assembly_name:Contig74"
196022. .200348
/note="assembly_name:Contig73"
200369. .202575
/note="assembly_name:Contig72"
202596. .203643
/note="assembly_name:Contig71"
203664. .204541
/note="assembly_name:Contig70"
204562. .204816
/note="assembly_name:Contig69"

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 40 Row: 0 Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13507671.

FEATURES

source

Location/Qualifiers
1. 1574
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="MGC:30824 IMAGE:3995193"
/tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMV."
/clone_lib="NCI CGAP_Lu29"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

gene

1. 1574
/gene="Gpr84"
/note="synonym: EX33"
/db_xref="LocusID:80910"
/db_xref="MGI:1934129"
147. 1337
/codon_start=1
/product="G protein-coupled receptor 84"
/protein_id="AAH23249.1"
/db_xref="GI:23273890"
/db_xref="LocusID:80910"
/translation="MNSSDANFSCYHESVLGRYFAVINGVAVAVTGVNVLTLA LAIRPKLRTRFNLLIANTLDTLLQFPFSDVTYHLHWRTGAVFCRIFGLLLFT SNSVSLTLCLIALGRYLLIAHPKLFQVESAKGIVLALGVSWVGVTSFAPLWNVFLVPVCTCSFDRMERGPYITLMGIYFVLGLSSVGFYCLIHQVRFAPARALDQYGLH QASIRSHOVAGTQEAHPGHFQELDSGVASRGSEGISSEPVSAATQTLEGDSSEAGG QGIRKAAQOIAERSLPEVHRKPRETAGARATDAPSEFGKVRMCFVFLCFALSYIP FLILLILDARGRPRVVMVAANLTWLNLCINPVLVYAMNRQFRHAYGSILKRGPOSF RRFH"

CDS

misc_feature

369. 818
/note="7tm_1; Region: 7 transmembrane receptor (rhodopsin family)"
/db_xref="CDD:pfam00001"

misc_feature

1032. 1256
/note="7tm_1; Region: 7 transmembrane receptor (rhodopsin family)"
/db_xref="CDD:pfam00001"

ORIGIN

Query Match 68.4%; Score 897; DB 10; Length 1574;
Best Local Similarity 83.9%; Pred. No. 2e-220;
Matches 1014; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

Qy	47	CTTTAGCCTCTATCATGTGGACAGCTCTGACGCCAACTTCCTCTGCTACCATGAGTCTG	106
Db	133	CCTCAGTCTCCATCATGTGGAACAGCTCAGATGCCAACTTCTCTGCTACCATGAGTCTG	192
Qy	107	TGCTGGGCTATCGTTATGTTGCAGTTAGTGGGGGTGGTGGTGTGACAGGACCG	166
Db	193	TGTTGGGCTATCGATACTTTGCAGTTATCTGGGCGTGGCAGTGGTGTGACAGGACCG	252
Qy	167	TGGCAATGTGCTCACCCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCA	226
Db	253	TGGGCAATGTGCTCACTCTGCTGGCCTTGGCCATTCTGTCCTCCCAAGCTCCGAACCCGCTCA	312

RESULT 12
AF272948 1611 bp mRNA linear ROD 06-APR-2001
LOCUS Mus musculus orphan G protein-coupled receptor 84 (Gpr84) mRNA, complete cds.
DEFINITION AF272948
ACCESSION AF272948
VERSION AF272948.1 GI:12711474
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1611)
AUTHORS Wittenberger,T., Schaller,H.C. and Hellebrand,S.
TITLE An expressed sequence tag (EST) data mining strategy succeeding in the discovery of new G-protein coupled receptors
JOURNAL J. Mol. Biol. 307 (3), 799-813 (2001)
MEDLINE 21172992
PUBMED 11273702
REFERENCE 2 (bases 1 to 1611)
AUTHORS Wittenberger,T. and Hellebrand,S.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2000) ZMNH, Institut fuer Entwicklungsneurobiologie, Martinistr. 52, Hamburg 20246, Germany
FEATURES
source
1..1611
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
1..1611
/gene="Gpr84"
138..1328
/gene="Gpr84"
/note="GPR84"
/codon_start=1
/product="orphan G protein-coupled receptor 84"
/protein_id="AAK01859.1"
/db_xref="GI:12711475"
/translation="MNWSSDANFSCYHESVLGYRYFAIIWGVAVAVTGVNVLTLA LAIRPKLRTRFNLIANLTADLLYCTLLQPSVDITYLHLWRTGAVFCRIEGLLLFT SNSVSIILTLCLIALGRYLLIAHPKLPQVFSAGKIVLALVGSWVGVTSFAPLWNVF LVPVVTCSFDRMRGRPYTILMGIYFVLGLSSGVFYCLIHROVKRAARALDQYGLH QASIRSHQVAGTQEAHPGFHQLDSDGVASRGPSEGISSEPVSAATQTLEGDSSEAG QGIRKAAQOIAERSLPEVHRKPRETAGARRATDAPSEFGKVTMCFAPVLCFALSYP FLILLNILDARGRAPRVVHMVAANLTWLNSCINPVLVYAAAMNRQFRAHAYGSILKRGPSF RRFH"
ORIGIN
Query Match 68.3%; Score 895.8; DB 10; Length 1611;
Best Local Similarity 83.7%; Pred. No. 4.1e-220;
Matches 1014; Conservative 0; Mismatches 197; Indels 0; Gaps 0;
QY 47 CTTTAGCCTCTATCATGTGGAACAGCTCTGACGCCAAGTCTCTCTGCTACCATGAGTCTG 106
Db 124 CCTCAGTCTCCATCATGTGGAACAGCTCAGATGCCAAGTCTCTCTGCTACCATGAGTCTG 183
QY 107 TGCTGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGTGGTGGTGGTGGTGGTGG 166
Db 184 TGTGGGCTATCGATACCTTTGCAATTATCTGGGGCGTGGCAGTGGCTGTGACAGGCACGG 243
QY 167 TGGGCAATGTGCTCACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCGATTCA 226
Db 244 TGGGCAATGTGCTCAGTCTGCTGGCCTTGGCCATTCGTCCTCAAGTCCGACCCGCTTCA 303
QY 227 ACCTGTTCATAGCCAACTCAGCTGAGTGGCTGATCTCTCTACTGACCGCTCTTCAGCCCT 286
Db 304 ACCTGTTCATAGCCAACTCAGCTGAGTGGCTGATCTACTACTGACCGCTCTTCAGCCCT 363
QY 287 TCTCTGTGGACACCTACCTCCACTGCACTGGCGCAGCGGTGCCACCTTCTGACGGGTAT 346
Db 364 TCTCGTGGACACATACCTCCACTCCACTTGGCGTACCGCGCGGTCTTCTGTAGATAT 423

QY 347 TTGGGCTCCTCCTTTTGGCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCAC 406
Db 424 TTGGACTCCTCCTCTTTTACTTCCAATTCTGTCTCCATCCTCACCCTCTGTCTCATGTCTC 483
QY 407 TGGGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCCAAGTTTTCAGTGCCAAAGG 466
Db 484 TAGGACGCTACCTCCTCATTTGCCACCCCTAAGCTCTTTCCCCAGGTTTTCAGTGCCAAAGG 543
QY 467 GGATAGTGTGGCAGCTGGTGAGCACCTGGGTTGTGGGGCTGGCCAGCTTTTGTCCCTCT 526
Db 544 GGATCGTGTGGCAGCTGGTGAGCACCTGGGTTGTGGGGCTGGCCAGCTTTTGTCCCTCT 603
QY 527 GGCCTATTATATCCTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCCGATCCGAGGCC 586
Db 604 GGAATGTTTGTCTTGGTGCCAGTTGTCTGCACCTTGACCTTGACCGCATGGAGGCC 663
QY 587 GGCCTTACACCACTCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCA 646
Db 664 GGCCTTACACCACTCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGCGTGGGCG 723
QY 647 TCTTCTATTGCCTCATCCACGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATACA 706
Db 724 TCTTCTACTGCTCATCCACCGCAAGTGAAGCGTGGGCTCGAGCACTGGACCAATACG 783
QY 707 AGTTGGCAGAGCAAGCATCCTACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTG 766
Db 784 GGCTGCATCAGGCCAGCATCCGCTCTCATCAGGTGGTGGGACACAAGAAGCCATGCCTG 843
QY 767 GTCGTTTCCAGGAGCTGGACAGCAGTTAGCATCAGGAGGACCCAGTGAAGGGGATTTTCAT 826
Db 844 GCCACTTCCAGGAGCTAGACAGCGGGGTTGCCCTCAGAGGGGCCAGCGAGGGGATTTTCAT 903
QY 827 CTGAGCCAGTCAAGTCTGCCACCAACCCAGACCCCTGGAGGGGACTCATCAGAAAGTGGGAG 886
Db 904 CTGAGCCAGTCAAGTCTGCCACCAACCCAGACCCCTGGAGGGTGAATTCGTAGAGTGGGG 963
QY 887 ACCAGATCAACAGCAAGAGAGTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTG 946
Db 964 GCCAGGCGATTAGAAAGGCGAGCTCAACAGATCGCAGAGAGAAGCCCTCCAGAAAGTGCATC 1023
QY 947 CCAAAGCCAGCCCAATTAAGGAGCCAGAAAGAGCTCCGGAATTTTCATCGGAAATTTGGGA 1006
Db 1024 GCAAGCCCCGGGAAACTGCAGAGCTCGCAGAGCCACAGATGCCCATCAGAGTTCGGGA 1083
QY 1007 AGGTGACTCGAATGTGTTTGTGCTGTGTTCTCTGCTTTCCTGAGCTACATCCCTTCT 1066
Db 1084 AGGTGACCCGTATGTGCTTCCAGTGTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143
QY 1067 TGCTGTCAACATTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTCTG 1126
Db 1144 TGTTGTCAACATTCTGGACGCCAGGGCCGCTGCTCCAGAGTAGTGACATGTTGGCTG 1203
QY 1127 CCAACCTCACCTGGCTCAATGGTTCATCAACCCCTGTCTCTATGCAGCCATGAACCGCC 1186
Db 1204 CCAACCTCACCTGGCTCAACAGCTGCATCAACCCCTGTCTCTATGCAGCCATGAACCGCC 1263
QY 1187 AATTCCGCCAAGCATATGGCTCCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCC 1246
Db 1264 AGTTCCGCCACGCGTATGGCTCCATCCTGAAACGCGGGGCCACAGAGTTTCCGCGGTTC 1323
QY 1247 ATTAGAACTGT 1257
Db 1324 ATTAAAGCTAT 1334

RESULT 13
AC126846
LOCUS AC126846 244845 bp DNA linear HTG 03-OCT-2002
DEFINITION Rattus norvegicus clone CH230-11M7, *** SEQUENCING IN PROGRESS ***.
ACCESSION AC126846
VERSION AC126846.2 GI:22772739
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 244845)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokereleh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

2 (bases 1 to 244845)
Worley,K.C.
Direct Submission
Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

REFERENCE

AUTHORS

TITLE

JOURNAL

3 (bases 1 to 244845)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (03-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Sep 10, 2002 this sequence version replaced gi:21722958.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the

sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only
contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GDTA

Center clone name: CH230-11M7

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 222716 bases at least Q40

Consensus quality: 225022 bases at least Q30

Consensus quality: 226487 bases at least Q20

Estimated insert size: 247241; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 244845: contig of 244845 bp in length.

FEATURES

source

1..244845

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-11M7"

1..1278

/note="wgs_contig"

1329..2694

/note="wgs_contig"

239866..241111

/note="wgs_contig"

243120..244845

/note="wgs_contig"

ORIGIN

Query Match 68.0%; Score 891; DB 2; Length 244845;

Best Local Similarity 82.1%; Pred. No. 6.3e-219;

Matches 1037; Conservative 0; Mismatches 225; Indels 1; Gaps 1;

QY 10 AGTTTCTGATTCCCTCTTCTCTCTCCACCCCTCTGCTCTTTAGCCTCTATCATGTGGAAC 69

Db 54626 AAGTTCTCATACATCTCCCTC-TCCCTCTCTCTCCCTTCAGTCTCCATCATGTGGAAC 54684

QY 70 AGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGTTATGTTGCA 129

Db 54685 AGCTCAGATGACAACTTCTCCTGCTACCATGAGTCTGTATTGGGCTATCGATACTTTGCA 54744

QY 130 GTTAGCTGGGGGTGGTGGTGTGTGACAGGCACCGTGGGCAATGTCTCACCCTACTG 189

Db 54745 GTTATCTGGGGCATGGTAGTGGTGTGCAACAGGCACCGTGGGCAATGTCTCACCCTGTTG 54804

QY 190 GCCTTGGCCATCCAGCCCAAGCTCCGTAACCGATTCAACCTGCTCATAGCCCACTCACA 249

Db 54805 GCCTTGGCCATCCGTCCTCCAAACTCCGAACCCGTTTCAACCTGCTCATAGCCCACTCACC 54864

QY 250 CTGGTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACCTACCTCCAC 309

Db 54865 CTGGTGATCTACTTACTGTACACGCTCCTGACGCCCTTCTCCGTTGGACACATACCTCCAC 54924

QY 310 CTGCACTGGCGCACCGGTGCCACCTTCTGAGGGTATTGTTGGGCTCCTCTTTTGCCTCC 369

Db 54925 CTCCATTGGCGCACGGCGCCATCTTCTGTAGATAATTCGGACTCCTCTTACTTCC 54984

QY 370 AATTCTGTCTCCATCTGTACCCCTCTGCTCATCGCACTGGGACGTACCTCTCTCATGGC 429

Db 54985 AATTCTGTCTCCATCTTACCCCTCTGTCTCATGCTCTAGGACGTACCTTCTCATGGC 55044

QY 430 CACCCTAAGCTTTTCCCCCAAGTTTTCAGTGCACCAAGGGATAGTCTGGCACTGGTGAGC 489

Db 55045 CACCCTAAGCTCTTCCCCAGGTTTTCAGTGCACCAAGGGATCGTCTGGCACTAGTGGC 55104

QY 490 ACCTGGGTTGTGGCGTGGCGGAGCTTTTGTCTCCCTCTGCTGCTATTTATATCCTGGTACT 549

Db 55105 AGCTGGGTTGTGGGGTGACACAGCTTTTGGCCCCCTCTGGAATGTTATGTCTTGGTGCA 55164

QY 550 GTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGGCGGCGCTTACACCACTCCTCATG 609

Db 55165 GTTGTCTGCACCTGCAGCTTTTGACCGCGTGGGAGGCGGCGCTTACACCACTCCTCATG 55224

QY 610 GGCACTACTTTGTGCTTGGGCTCAGACGTGTGGCATCTTCTATTTGCTCCTCATCCGCG 669

Db 55225 GGCACTCTTGTGCTTGGGCTCAGACGTGTGGCGCTTCTTACTGCTCATCCACCGC 55284

QY 670 CAGGTCAACAGCAGCAGCAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCAGTGTGCCACC 849

Db 55285 CAAGTGAAGCTGCGGCTCGAGCGTGCACAAATATGGGCTGAGGAGGCGCAGCATGCGC 55344

QY 730 TCCAAACATGTGGCCAGGACTGATGAGGCCATGCTGCTGCTTCCAGGAGCTGGACAGC 789

Db 55345 TCCCATCAGGTGTGGGACACATGAAGCTGTGCCAGGCCACTTCCAGGAGCTAGACAGC 55404

QY 790 AGGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCAGTGTGCCACC 849

Db 55405 GGGCTTGATCAAGAGGTCCAGCGAAGGGATTTTCATCTGAGCCAGTCAGTGTGCCAGC 55464

QY 850 ACCCAGACCTCGAAGGGGACTCATCAGAAAGTGGGAGACCAAGATCAACAGCAAGAGAGCT 909

Db 55465 ACACAGACCTCGAAGGTGATTCGTGAGAAAGCGGGGACCGGCGATGAGAAAGGAGCT 55524

QY 910 AAGCAGATGCGAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCAAATTAAGGA 969

Db 55525 CAGCAGATCTCAGAGAGAGAGCCCTTCAGAAAGTGCATCGCAAGACTGGAGGAGCTGAGGA 55584

QY 970 GCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGTGTGACTCGAATGTGTTTGTCT 1029

Db 55585 GCACGCAGAGCCACGGATGCACCATCGGAGTTCGGGAAGTGTGACCCGTATGTGCTTGCA 55644

QY 1030 GTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATTCCTGATGCC 1089

Db 55645 GTGTTCTTGTCTTCTGCTCAGCTACATCCCTTCTTGTGCTCAACATTCCTGAGGCC 55704

QY 1090 AGATCCAGGCTCCCGGGTGGTCCACATGCTTGTGTCACCACTCCTGCTCAATGGT 1149

Db 55705 AGGGCGCGCTCCACGAGTAGTGCATATGTTGTGTCGCAACCTCCTGCTCAACAGC 55764

QY 1150 TGCATCAACCTGTGCTCTATGAGCCATGAACCGCCATTCGCGCAAGCATATGGCTCC 1209

Db 55765 TGCATCAACCTGTGCTCTATGAGCCATGAACCGCCATTCGCGCAAGCTATGGCTCC 55824

QY 1210 ATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATAGAACTGTGACCTAGTAC 1269

Db 55825 ATCTGAAACGCGGGCCACAGAGTTTCCGACGGTTCCATTAGAGCTAGTAGTCCACTCAC 55884

QY 1270 CAG 1272

Db 55885 CAG 55887

RESULT 14
AC016463
LOCUS
DEFINITION Homo sapiens clone RP11-1009, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC016463

AC016463 141003 bp DNA linear HTG 13-JUL-2000

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

AC016463.3 GI:7144792
HTG; HTGS_PHASE0.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 141003)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-1009
Unpublished
2 (bases 1 to 141003)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (30-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:6910791.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: I3130

Center clone name: 10_O_9

* NOTE: This record contains 152 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 865: contig of 865 bp in length
* 866 965: gap of 100 bp
* 966 1849: contig of 884 bp in length
* 1850 1949: gap of 100 bp
* 1950 2856: contig of 907 bp in length
* 2857 2956: gap of 100 bp
* 2957 3860: contig of 904 bp in length
* 3861 3960: gap of 100 bp
* 3961 4824: contig of 864 bp in length
* 4825 5792: contig of 868 bp in length
* 5793 5892: gap of 100 bp
* 5893 6794: contig of 901 bp in length
* 6794 6893: gap of 100 bp
* 6894 7790: contig of 897 bp in length
* 7791 7890: gap of 100 bp
* 7891 8752: contig of 862 bp in length
* 8753 9726: gap of 100 bp
* 8853 9727: contig of 874 bp in length
* 9727 9826: gap of 100 bp
* 9827 10727: contig of 901 bp in length

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: September 23, 2004, 22:02:34 ; Search time 591.574 Seconds
(without alignments)
9414.519 Million cell updates/sec

Title: US-10-029-436-1
Perfect score: 1311
Sequence: 1 ttgaatgctaggttctgtatt.....caggaccaaaagtgccaggta 1311
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB ID	Description
		Match	Length		
1	1311	100.0	1311	8 ACC84331	Acc84331 Human hpl
2	1306	99.6	2046	4 AAS28996	Aas28996 Genomic s
3	1306	99.6	2046	4 AAS30237	Aas30237 DNA encod
4	1306	99.6	2046	4 AAS35064	Aas35064 DNA #14 e
5	1306	99.6	2046	4 AAK77581	Aak77581 Human imm
6	1306	99.6	2046	4 ABA06789	Aba06789 Human gen
7	1306	99.6	2046	4 ABK44021	Abk44021 Genomic D
8	1306	99.6	2046	5 AAS29737	Aas29737 Human end
9	1306	99.6	2046	6 ABT07831	Abt07831 Novel hum
10	1306	99.6	2046	6 ABV84126	Abv84126 Human pol
11	1306	99.6	2046	7 ACD01492	Acd01492 Human gen
12	1306	99.6	2046	9 ADC46506	Adc46506 Human neo
13	1306	99.6	5460	6 AAI68792	Aai68792 Human MAR
14	1256.4	95.8	1498	2 AAV38513	Aav38513 Human 7-t
15	1256.4	95.8	1546	6 AAS98070	Aas98070 Human DNA
16	1256.4	95.8	1546	7 ABT17029	Abt17029 Human MP2
17	1256.4	95.8	1546	7 ABZ42551	Abz42551 Human G p
18	1256.4	95.8	1595	4 AAH78712	Aah78712 Human EX3
19	1255.6	95.8	1579	4 AAI99548	Aai99548 Human exp
20	1227	93.6	1227	6 AAI68793	Aai68793 Human MAR
21	1219.4	93.0	1416	4 AAK77579	Aak77579 Human imm
22	1191	90.8	1191	6 ABZ42892	Abz42892 Human GPC
23	1188	90.6	1188	7 ABV73365	Abv73365 Human TGR

24	887.6	67.7	1191	7 ABV73374	Abv73374 Mouse TGR
25	840	64.1	840	6 AAS98133	Aas98133 Human DNA
26	684.6	52.2	712	4 AAK77580	Aak77580 Human imm
27	360.4	27.5	485	6 ABL89786	Ab189786 Human pol
28	355	27.1	483	4 AAS28939	Aas28939 cDNA enco
29	355	27.1	483	4 AAS30167	Aas30167 DNA enco
30	355	27.1	483	4 AAS34782	Aas34782 cDNA enco
31	355	27.1	483	4 AAI99575	Aai99575 Human exp
32	355	27.1	483	4 ABA06396	Aba06396 Human cDN
33	355	27.1	483	4 ABK43453	Abk43453 DNA enco
34	355	27.1	483	5 AAS29521	Aas29521 Human end
35	355	27.1	483	6 ABT07774	Abt07774 Novel hum
36	355	27.1	483	6 ABV83733	Abv83733 Human pol
37	355	27.1	483	7 ACD01422	Acd01422 Human pol
38	355	27.1	483	9 ADC45940	Adc45940 Human neo
39	346.2	26.4	347	4 AAK60376	Aak60376 Human imm
40	87.8	6.7	1382	3 AAZ51461	Aaz51461 Human G p
41	87.8	6.7	1382	7 ADA19230	Ada19230 Human ins
42	87.8	6.7	1382	7 ABZ42815	Abz42815 Human G p
43	87.8	6.7	1382	8 ADB67667	Adb67667 Human G-p
44	87.8	6.7	1584	2 AAV37701	Aav37701 Human his
45	87.8	6.7	1584	7 ACA55686	Aca55686 Signallin

ALIGNMENTS

RESULT 1
ACC84331
ID ACC84331 standard; DNA; 1311 BP.
XX
AC ACC84331;
XX
DT 03-OCT-2003 (first entry)
XX Human hpl5a receptor coding sequence.
DE
KW Human; hpl5a; receptor; G-protein coupled receptor; cardiant;
KW gastrointestinal; gene therapy; gene; ds.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 61..1251
FT /*tag= a
FT /product= "hpl5a"
XX
PN WO2003054540-A1.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US040612.
XX
PR 19-DEC-2001; 2001US-00029436.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Smith KE, Weinshank R;
XX
DR WPI; 2003-559173/52.
DR P-PSDB; ABR52422.
XX
PT New recombinant nucleic acid, useful for preparing a composition for
PT treating disorders linked to human hpl5a receptor e.g. cardiovascular or
PT gastrointestinal disorders.
XX
PS Claim 1; Fig 1A-B; 98pp; English.
XX
CC The present sequence is that of nucleic acid encoding a human orphan G-
CC protein coupled receptor, designated hpl5a. The sequence was initially
CC identified in a human placenta genomic library using probes representing
CC transmembrane domains Iii, V and VI of human serotonin 5-Hy1Dbeta
CC receptor. The endogenous ligand for hpl5a is likely to be a

PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-488777/53.

New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Disclosure; SEQ ID NO 130; 524pp; English.

The present invention relates to the isolation of novel human uterine motility-association polypeptides (AAU18094-AAU18152), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAS28995-AAS29020 represent genomic sequences encoding for novel human uterine motility-association polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at:ftp.wipo.int/pub/published_pct_sequences

Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;

Query Match 99.6%; Score 1306; DB 4; Length 2046;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGAATGCTAGGTTCTGATTCCCTCTTCCTCTTCCACCCTCTGCCTCTTAGCCTCTATC 60

PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.

PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-488787/53.

PT New polynucleotides and polypeptides, useful for diagnosing, treating,
PT preventing or prognosing e.g. kidney, cardiovascular, blood, electrolyte
PT imbalance or neoplastic disorders, autoimmune diseases, cancers.

PS Claim 1; SEQ ID NO 155; 506pp; English.

XX The invention relates to novel nucleic acids and polypeptides useful for
CC diagnosing, treating, preventing and/or prognosing disorders related to
CC these polypeptides. The polynucleotides are especially useful in the
CC diagnosis, prognosis, prevention and/or treatment of diseases which
CC include kidney disorders (e.g. renal failure or nephritis),
CC cardiovascular disorders (e.g. hypertension or myocardial infarction),
CC blood disorders (e.g. anaemia or blood coagulation disorders),
CC electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia),
CC neoplastic disorders (e.g. nephroma or renal cell cancer), autoimmune
CC diseases, cancers, inflammatory diseases, reproductive system disorders,
CC endocrine disorders, neural activity and neurological disorders, wound
CC healing and respiratory disorders. AAS30165-AAS30251 represent the novel
CC human renal and cardiovascular-associated nucleic acid sequences of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at: ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;

Query Match 99.6%; Score 1306; DB 4; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATGCTAGTCTTGATTCCTCTCTCCCTCTCCACCCCTCTGCCTTTAGCCTCTATC 60
DB 577 TTGAATGCTAGTCTTGATTCCTCTCTCCCTCTCCACCCCTCTGCCTTTAGCCTCTATC 636

QY 61 ATGTGGAACAGCTCTGACGCCAACHTCTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 120
Db 637 ATGTGGAACAGCTCTGACGCCAACHTCTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 696
QY 121 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGSACCGTGGGCAATGTGCTC 180
Db 697 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGSACCGTGGGCAATGTGCTC 756
QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGANTCAACCTGCTCATAGCC 240
Db 757 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGANTCAACCTGCTCATAGCC 816
QY 241 AACCTCAGACTGGCTGATCTCCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACACC 300
Db 817 AACCTCAGACTGGCTGATCTCCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACACC 876
QY 301 TACCTCCACCTGCACCTGGCGCACCGTGCCACCTTCTGCAAGGTATTTGGGCTCCTCCTT 360
Db 877 TACCTCCACCTGCACCTGGCGCACCGTGCCACCTTCTGCAAGGTATTTGGGCTCCTCCTT 936
QY 361 TTTGCTTCCAAATCTGTCTCCATCTGACCTCTGCTCTCATCGCACTGGGACGCTACCTC 420
Db 937 TTTGCTTCCAAATCTGTCTCCATCTGACCTCTGCTCTCATCGCACTGGGACGCTACCTC 996
QY 421 CTCATTGCCACCCCTAAGCTTTTCCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 480
Db 997 CTCATTGCCACCCCTAAGCTTTTCCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 1056
QY 481 CTGGTGAGACCTGGGTTGTGGGCTGGCCAGCTTTTGCTCCCTCTGGCCCTATTATATC 540
Db 1057 CTGGTGAGACCTGGGTTGTGGGCTGGCCAGCTTTTGCTCCCTCTGGCCCTATTATATC 1116
QY 541 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCAGGCCGGCCTTACACCACC 600
Db 1117 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCAGGCCGGCCTTACACCACC 1176
QY 601 ATCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTCGCTC 660
Db 1177 ATCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTCGCTC 1236
QY 661 ATCCACCGCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 720
Db 1237 ATCCACCGCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 1296
QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGCTTCCAGGAG 780
Db 1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGCTTCCAGGAG 1356
QY 781 CTGGACAGCAGGTTAGCATCAGGAGACCCAGTGAAGGGAATTCATCTGAGCCAGTCAGT 840
Db 1357 CTGGACAGCAGGTTAGCATCAGGAGACCCAGTGAAGGGAATTCATCTGAGCCAGTCAGT 1416
QY 841 GCTGCCACACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 900
Db 1417 GCTGCCACACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 1476
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 960
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 1536
QY 961 ATTAAGGAGCCAGAGAGCTCCGGATTTCTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
Db 1537 ATTAAGGAGCCAGAGAGCTCCGGATTTCTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
QY 1021 TGTGTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1080
Db 1597 TGTGTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1656
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGTGCTGCCAACCTCACCTGG 1140
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGTGCTGCCAACCTCACCTGG 1716
QY 1141 CTCAATGTTGTCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCGCCCAAGCA 1200

Db 1717 CTCAATGTTGTCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCGCCCAAGCA 1776
QY 1201 TATGGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1260
Db 1777 TATGGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1836
QY 1261 CCTAGTCACCAGAATTTCAGGACTGTCTCTCTCCAGGACCAAAAGTGGC 1306
Db 1837 CCTAGTCACCAGAATTTCAGGACTGTCTCTCTCCAGGACCAAAAGTGGC 1882
RESULT 4
AAS35064
ID AAS35064 standard; DNA; 2046 BP.
XX AAS35064;
AC AAS35064;
XX AC
DT 04-DEC-2001 (first entry)
XX 04-DEC-2001 (first entry)
DE DNA #14 encoding human neoplastic disease associated polypeptide.
XX Human; neoplastic disease associated polypeptide; cancer; gene therapy;
KW hyperproliferative disorder; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic; ds.
XX
OS Homo sapiens.
XX
PN WO200155163-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001358.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.

PR	01-SEP-2000;	2000US-02293433P;
PR	01-SEP-2000;	2000US-02293444P;
PR	01-SEP-2000;	2000US-02293455P;
PR	05-SEP-2000;	2000US-02295095P;
PR	05-SEP-2000;	2000US-02295133P;
PR	06-SEP-2000;	2000US-0230437P;
PR	06-SEP-2000;	2000US-0230438P;
PR	08-SEP-2000;	2000US-02312423P;
PR	08-SEP-2000;	2000US-02312433P;
PR	08-SEP-2000;	2000US-02312444P;
PR	08-SEP-2000;	2000US-02314133P;
PR	08-SEP-2000;	2000US-02314144P;
PR	08-SEP-2000;	2000US-0232080P;
PR	08-SEP-2000;	2000US-02320811P;
PR	12-SEP-2000;	2000US-0231968P;
PR	14-SEP-2000;	2000US-0232397P;
PR	14-SEP-2000;	2000US-0232398P;
PR	14-SEP-2000;	2000US-0232399P;
PR	14-SEP-2000;	2000US-0232400P;
PR	14-SEP-2000;	2000US-0232401P;
PR	14-SEP-2000;	2000US-02324063P;
PR	14-SEP-2000;	2000US-0233064P;
PR	14-SEP-2000;	2000US-0233065P;
PR	21-SEP-2000;	2000US-02342233P;
PR	21-SEP-2000;	2000US-0234274P;
PR	25-SEP-2000;	2000US-0234997P;
PR	25-SEP-2000;	2000US-0234998P;
PR	26-SEP-2000;	2000US-0235484P;
PR	27-SEP-2000;	2000US-0235834P;
PR	27-SEP-2000;	2000US-0235836P;
PR	29-SEP-2000;	2000US-0236327P;
PR	29-SEP-2000;	2000US-0236367P;
PR	29-SEP-2000;	2000US-0236368P;
PR	29-SEP-2000;	2000US-0236369P;
PR	29-SEP-2000;	2000US-0236370P;
PR	02-OCT-2000;	2000US-0236802P;
PR	02-OCT-2000;	2000US-0237037P;
PR	02-OCT-2000;	2000US-0237038P;
PR	02-OCT-2000;	2000US-0237039P;
PR	02-OCT-2000;	2000US-0237040P;
PR	13-OCT-2000;	2000US-0239935P;
PR	13-OCT-2000;	2000US-0239937P;
PR	20-OCT-2000;	2000US-0240960P;
PR	20-OCT-2000;	2000US-0241221P;
PR	20-OCT-2000;	2000US-0241785P;
PR	20-OCT-2000;	2000US-0241786P;
PR	20-OCT-2000;	2000US-0241787P;
PR	20-OCT-2000;	2000US-0241808P;
PR	20-OCT-2000;	2000US-0241809P;
PR	20-OCT-2000;	2000US-0241826P;
PR	01-NOV-2000;	2000US-0244617P;
PR	08-NOV-2000;	2000US-0246474P;
PR	08-NOV-2000;	2000US-0246475P;
PR	08-NOV-2000;	2000US-0246476P;
PR	08-NOV-2000;	2000US-0246477P;
PR	08-NOV-2000;	2000US-0246478P;
PR	08-NOV-2000;	2000US-02465233P;
PR	08-NOV-2000;	2000US-0246524P;
PR	08-NOV-2000;	2000US-0246525P;
PR	08-NOV-2000;	2000US-0246526P;
PR	08-NOV-2000;	2000US-0246527P;
PR	08-NOV-2000;	2000US-0246528P;
PR	08-NOV-2000;	2000US-0246532P;
PR	08-NOV-2000;	2000US-0246609P;
PR	08-NOV-2000;	2000US-0246610P;
PR	08-NOV-2000;	2000US-0246611P;
PR	08-NOV-2000;	2000US-0246613P;
PR	17-NOV-2000;	2000US-0249207P;
PR	17-NOV-2000;	2000US-0249208P;
PR	17-NOV-2000;	2000US-0249209P;
PR	17-NOV-2000;	2000US-0249210P;
PR	17-NOV-2000;	2000US-0249212P;

PR	17-NOV-2000;	2000US-0249213P.
PR	17-NOV-2000;	2000US-0249214P.
PR	17-NOV-2000;	2000US-0249215P.
PR	17-NOV-2000;	2000US-0249216P.
PR	17-NOV-2000;	2000US-0249217P.
PR	17-NOV-2000;	2000US-0249218P.
PR	17-NOV-2000;	2000US-0249244P.
PR	17-NOV-2000;	2000US-0249245P.
PR	17-NOV-2000;	2000US-0249264P.
PR	17-NOV-2000;	2000US-0249265P.
PR	17-NOV-2000;	2000US-0249297P.
PR	17-NOV-2000;	2000US-0249299P.
PR	17-NOV-2000;	2000US-0249300P.
PR	01-DEC-2000;	2000US-0250160P.
PR	01-DEC-2000;	2000US-0250319P.
PR	05-DEC-2000;	2000US-0251030P.
PR	05-DEC-2000;	2000US-0251988P.
PR	05-DEC-2000;	2000US-0256719P.
PR	06-DEC-2000;	2000US-0251479P.
PR	08-DEC-2000;	2000US-0251856P.
PR	08-DEC-2000;	2000US-0251868P.
PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251989P.
PR	08-DEC-2000;	2000US-0251990P.
PR	11-DEC-2000;	2000US-0254097P.
PR	05-JAN-2001;	2001US-0259678P.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI; 2001-465558/50.	

Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis.

Disclosure: SEQ ID NO 592; 687pp; English.

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, muscular disorders, cardiovascular disorders and renal disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAS35051-AAS35125 represent DNA sequences encoding for the novel human neoplastic disease associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct_sequences

Query Match 99.6%; Score 1306; DB 4; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;

QY	1	TTGAATGCTAGGTTCTGAATCCCTCTCTTCCCTCTCCACCCCTCTGCCTCTTTAGCCCTCTATC	60
DB	577	TTGAATGCTAGGTTCTGAATCCCTCTCTTCCCTCTTCCACCCCTCTGCCTCTTTAGCCCTCTATC	636
QY	61	ATGTGGAACAGCTCTGACGCCAAACTTCTCCTGCTACCAATGAGTCTGTGCTGGGCTATCGT	120
DB	637	ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCAATGAGTCTGTGCTGGGCTATCGT	696
QY	121	TATGTTGCAGTTAGCTGGGGGGTGGTGGTGGCTGTGACAGSCACCGTGGGCAATGTGCTC	180

Db 697 TAATGTTGCAAGTTAGTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 756

QY 181 ACCCTACTGGCCCTTGGCCATCCAGCCAAAGCTCCGTACCCGATTAACCTGCTCATAGCC 240

Db 757 ACCCTACTGGCCCTTGGCCATCCAGCCAAAGCTCCGTACCCGATTAACCTGCTCATAGCC 816

QY 241 AACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACACC 300

Db 817 AACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACACC 876

QY 301 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 360

Db 877 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 936

QY 361 TTTGCCCTCAATTTCTGTCTCCATCTGTACCTCTGACCTCTGCTCATCGCACTGGGACGCTACCTC 420

Db 937 TTTGCCCTCAATTTCTGTCTCCATCTGTACCTCTGACCTCTGCTCATCGCACTGGGACGCTACCTC 996

QY 421 CTCATTGCCACCCCTAAGCTTTTCCCCCAAGTTTTCAGTGCCAAAGGGATAGTGTGGCA 480

Db 997 CTCATTGCCACCCCTAAGCTTTTCCCCCAAGTTTTCAGTGCCAAAGGGATAGTGTGGCA 1056

QY 481 CTGGTGACCACTGGGTGTGGGGGTGGGCCAGCTTTTGTCTCCCTCTGGCCTATTATATC 540

Db 1057 CTGGTGACCACTGGGTGTGGGGGTGGGCCAGCTTTTGTCTCCCTCTGGCCTATTATATC 1116

QY 541 CTGGTACTGTAGTCTGCACCTGTGAGCTTTTGACCGCATCCGAGGCGGCTTACACCAACC 600

Db 1117 CTGGTACTGTAGTCTGCACCTGTGAGCTTTTGACCGCATCCGAGGCGGCTTACACCAACC 1176

QY 601 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATGCTCCTC 660

Db 1177 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATGCTCCTC 1236

QY 661 ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 720

Db 1237 ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 1296

QY 721 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTTCCAGGAG 780

Db 1297 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTTCCAGGAG 1356

QY 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGATTTTCTATGAGCCAGTCACT 840

Db 1357 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGATTTTCTATGAGCCAGTCACT 1416

QY 841 GCTGCCACCAACCCAGACCCCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 900

Db 1417 GCTGCCACCAACCCAGACCCCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 1476

QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 960

Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 1536

QY 961 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTATCGGAATTTGGGAGGTGACTCGAATG 1020

Db 1537 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTATCGGAATTTGGGAGGTGACTCGAATG 1596

QY 1021 TGTGTTGTGTGTTCTCTGCTTTGCCCCCTGAGCTACATCCCTTCTTGTCTGCTCAACATT 1080

Db 1597 TGTGTTGTGTGTTCTCTGCTTTGCCCCCTGAGCTACATCCCTTCTTGTCTGCTCAACATT 1656

QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1140

Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1716

QY 1141 CTCAATGGTTGCATCAACCTGTGCTCTATGACGCCATGAACCGCCAAATTCGCCCAAGCA 1200

Db 1717 CTCAATGGTTGCATCAACCTGTGCTCTATGACGCCATGAACCGCCAAATTCGCCCAAGCA 1776

QY 1201 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTTAGAACTGTGAC 1260

Db 1777 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTTAGAACTGTGAC 1836

QY 1261 CCTAGTCACCAGAATTTCAGGACTGTCTCTCCAGGACCAAAAGTGGC 1306

Db 1837 CCTAGTCACCAGAATTTCAGGACTGTCTCTCCAGGACCAAAAGTGGC 1882

RESULT 5

AAK77581

ID AAK77581 standard; DNA; 2046 BP.

XX AAK77581;

AC AC

XX XX

DT 07-NOV-2001 (first entry)

XX

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32393.

XX

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

KW cytostatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

OS

XX

PN WO200157182-A2.

XX

PD 09-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US001354.

XX

PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.

PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
DR
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
PS Disclosure; SEQ ID NO 32393; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins, and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;

Query Match 99.6%; Score 1306; DB 4; Length 2046;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATGCTAGGTTCTGATTCCTCTTCTCTTCCACCCCTCTGCCCTCTTTAGCCTCTATC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
577 TTGAATGCTAGGTTCTGATTCCTCTTCTCTTCCACCCCTCTGCCCTCTTTAGCCTCTATC 636
QY 61 ATGTGGAACAGCTCTGACGCCAACTTCTCTCTGCTACCATGAGTCTGTGGCTATCGT 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
637 ATGTGGAACAGCTCTGACGCCAACTTCTCTCTGCTACCATGAGTCTGTGGCTATCGT 696
QY 121 TATGTTGCAGTTAGTGGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
697 TATGTTGCAGTTAGTGGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 756
QY 181 ACCCTACTGGCCTTGGCCCATCCAGCCCCAAGCTCCGTACCCGATTCACTGCTCATAGCC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
757 ACCCTACTGGCCTTGGCCCATCCAGCCCCAAGCTCCGTACCCGATTCACTGCTCATAGCC 816
QY 241 AACCTCACACTGGTGTATCTCCTCTACTGACCGCTCCTTTCAGCCCTTCTCTGTGGACACC 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
817 AACCTCACACTGGTGTATCTCCTCTACTGACCGCTCCTTTCAGCCCTTCTCTGTGGACACC 876

QY	601	ATCCTCATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC	660	PN	WO200155318-A2.	
Db	1177	ATCCTCATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC	1236	XX	02-AUG-2001.	
QY	661	ATCCACCGCCAGGTCAAACGAGCAGCAGGCACCTGGACCAATACAAGTTGCGACAGGCA	720	PF	17-JAN-2001; 2001WO-US0001332.	
Db	1237	ATCCACCGCCAGGTCAAACGAGCAGCAGGCACCTGGACCAATACAAGTTGCGACAGGCA	1296	XX	31-JAN-2000; 2000US-0179065P.	
QY	721	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTGTTCCAGGAG	780	PR	04-FEB-2000; 2000US-0180628P.	
Db	1297	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTGTTCCAGGAG	1356	PR	24-FEB-2000; 2000US-0184664P.	
QY	781	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT	840	PR	02-MAR-2000; 2000US-0186350P.	
Db	1357	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT	1416	PR	16-MAR-2000; 2000US-0189874P.	
QY	841	GCTGCCACCAACCCAGACCCCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC	900	PR	17-MAR-2000; 2000US-0190076P.	
Db	1417	GCTGCCACCAACCCAGACCCCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC	1476	PR	18-APR-2000; 2000US-0198123P.	
QY	901	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGGCCA	960	PR	19-MAY-2000; 2000US-0205515P.	
Db	1477	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGGCCA	1536	PR	07-JUN-2000; 2000US-0209467P.	
QY	961	ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	1020	PR	28-JUN-2000; 2000US-0214886P.	
Db	1537	ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	1596	PR	30-JUN-2000; 2000US-0215135P.	
QY	1021	TGTTTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT	1080	PR	07-JUL-2000; 2000US-0216880P.	
Db	1597	TGTTTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT	1656	PR	11-JUL-2000; 2000US-0217487P.	
QY	1081	CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG	1140	PR	11-JUL-2000; 2000US-0217496P.	
Db	1657	CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG	1716	PR	14-JUL-2000; 2000US-0218290P.	
QY	1141	CTCAATGTTGTCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCGCGCAAGCA	1200	PR	26-JUL-2000; 2000US-0220964P.	
Db	1717	CTCAATGTTGTCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCGCGCAAGCA	1776	PR	14-AUG-2000; 2000US-0224518P.	
QY	1201	TATGGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC	1260	PR	14-AUG-2000; 2000US-0224519P.	
Db	1777	TATGGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC	1836	PR	14-AUG-2000; 2000US-0225214P.	
QY	1261	CCTAGTACCAGAAATTCAGGACTGTCTCTCTCCAGGACCAAAAGTGGC	1306	PR	14-AUG-2000; 2000US-0225266P.	
Db	1837	CCTAGTACCAGAAATTCAGGACTGTCTCTCTCCAGGACCAAAAGTGGC	1882	PR	14-AUG-2000; 2000US-0225267P.	
RESULT 7					PR	14-AUG-2000; 2000US-0225268P.
ABK44021					PR	14-AUG-2000; 2000US-0225270P.
ID	ABK44021 standard; DNA; 2046 BP.				PR	14-AUG-2000; 2000US-0225447P.
XX					PR	14-AUG-2000; 2000US-0225757P.
AC	ABK44021;				PR	14-AUG-2000; 2000US-0225758P.
XX					PR	14-AUG-2000; 2000US-0225759P.
DT	05-JUN-2002 (first entry)				PR	18-AUG-2000; 2000US-0226279P.
XX					PR	22-AUG-2000; 2000US-0226681P.
DE	Genomic DNA encoding novel central nervous system protein #33.				PR	22-AUG-2000; 2000US-0226868P.
XX					PR	23-AUG-2000; 2000US-0227009P.
KW	Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;				PR	30-AUG-2000; 2000US-0228924P.
KW	hyperproliferative disorder; neoplasm; cardiovascular disorder;				PR	01-SEP-2000; 2000US-0229287P.
KW	cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;				PR	01-SEP-2000; 2000US-0229343P.
KW	nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;				PR	01-SEP-2000; 2000US-0229344P.
KW	acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;				PR	01-SEP-2000; 2000US-0229345P.
KW	adenocarcinoma; reproductive system disorder; testicular feminisation;				PR	05-SEP-2000; 2000US-0229509P.
KW	endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;				PR	05-SEP-2000; 2000US-0229513P.
KW	respiratory disorder; renal disorder; kidney failure; blood disorder;				PR	06-SEP-2000; 2000US-0230437P.
KW	myocardial infarction; wound healing; cell proliferation; skin aging;				PR	06-SEP-2000; 2000US-0230438P.
XX	food additive; food preservative; gene therapy; gene; ds.				PR	08-SEP-2000; 2000US-0231242P.
OS	Homo sapiens.				PR	08-SEP-2000; 2000US-0231243P.
XX					PR	08-SEP-2000; 2000US-0231244P.
XX					PR	08-SEP-2000; 2000US-0231413P.
XX					PR	08-SEP-2000; 2000US-0231414P.
XX					PR	08-SEP-2000; 2000US-0232080P.
XX					PR	08-SEP-2000; 2000US-0232081P.
XX					PR	12-SEP-2000; 2000US-0231968P.
XX					PR	14-SEP-2000; 2000US-0232397P.
XX					PR	14-SEP-2000; 2000US-0232398P.
XX					PR	14-SEP-2000; 2000US-0232399P.
XX					PR	14-SEP-2000; 2000US-0232400P.
XX					PR	14-SEP-2000; 2000US-0232401P.
XX					PR	14-SEP-2000; 2000US-0233063P.
XX					PR	14-SEP-2000; 2000US-0233064P.
XX					PR	14-SEP-2000; 2000US-0233065P.
XX					PR	21-SEP-2000; 2000US-0234223P.
XX					PR	21-SEP-2000; 2000US-0234274P.
XX					PR	25-SEP-2000; 2000US-0234997P.
XX					PR	25-SEP-2000; 2000US-0234998P.
XX					PR	26-SEP-2000; 2000US-0235484P.
XX					PR	27-SEP-2000; 2000US-0235834P.
XX					PR	27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
XX
PI

XX WPI; 2001-581633/65.
DR
XX
PT New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
PT
XX
PS Disclosure; SEQ ID NO 1209; 837pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional

Query Match 99.6%; Score 1306; DB 4; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGAATGCTAGGTTCTGATTCCTCTTCCTCTTCCACCCCTCTGCCCTTTAGCCTCTATC 60
Db |||||
577 TTGAATGCTAGGTTCTGATTCCTCTTCCTCTTCCACCCCTCTGCCCTTTAGCCTCTATC 636
QY 61 ATGTGGAACAGCTCTGACGGCAACTTCTCTGTCTACCATGAGTCTGTCTGGGCTATCGT 120
Db |||||
637 ATGTGGAACAGCTCTGACGGCAACTTCTCTGTCTACCATGAGTCTGTCTGGGCTATCGT 696
QY 121 TATGTTGCAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGCAACCGTGGGCAATGTGCTC 180
Db |||||
697 TATGTTGCAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGCAACCGTGGGCAATGTGCTC 756
QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGTCTCATAGCC 240
Db |||||
757 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGTCTCATAGCC 816
QY 241 AACCTCACACTGGCTGATCTCCTCTACTGCACGGTCTCTTACGCCCTTCTCTGTGGACACC 300
Db |||||
817 AACCTCACACTGGCTGATCTCCTCTACTGCACGGTCTCTTACGCCCTTCTCTGTGGACACC 876
QY 301 TACCTCCACCTGCCTGGGGCCACCGGTGCCACCTTCTGCAGGGTATTGGGCTCCTCCTT 360
Db |||||
877 TACCTCCACCTGCCTGGGGCCACCGGTGCCACCTTCTGCAGGGTATTGGGCTCCTCCTT 936
QY 361 TTTGCCCTCCAAATTCGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 420
Db |||||
937 TTTGCCCTCCAAATTCGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 996
QY 421 CTCATTGCCCCACCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA 480
Db |||||
997 CTCATTGCCCCACCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA 1056
QY 481 CTGGTGAGCACCTGGGTTGTGGGGCGTGGCCAGCTTTGCTCCCCCTCTGGCCTATTATATC 540
Db |||||
1057 CTGGTGAGCACCTGGGTTGTGGGGCGTGGCCAGCTTTGCTCCCCCTCTGGCCTATTATATC 1116

QY 541 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGCCTTACACCACC 600
Db |||||||
1117 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGCCTTACACCACC 1176
QY 601 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 660
Db |||||||
1177 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 1236
QY 661 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 720
Db |||||||
1237 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 1296
QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGGCTGTGTTCCAGGAG 780
Db |||||||
1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGGCTGTGTTCCAGGAG 1356
QY 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCAGT 840
Db |||||||
1357 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCAGT 1416
QY 841 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 900
Db |||||||
1417 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 1476
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCCAAGCA 960
Db |||||||
1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCCAAGCA 1536
QY 961 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGTGACTCGAATG 1020
Db |||||||
1537 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGTGACTCGAATG 1596
QY 1021 TGTGTTGCTGTGTTCTCTGCTTTGCTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1080
Db |||||||
1597 TGTGTTGCTGTGTTCTCTGCTTTGCTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1656
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCTCAACCTCGG 1140
Db |||||||
1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCTCAACCTCGG 1716
QY 1141 CTCAATGTTGCTATCAACCTGTGCTCTATGAGCCATGAACCGCAATTCGGCCCAAGCA 1200
Db |||||||
1717 CTCAATGTTGCTATCAACCTGTGCTCTATGAGCCATGAACCGCAATTCGGCCCAAGCA 1776
QY 1201 TATGGCTCATTATTTAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1260
Db |||||||
1777 TATGGCTCATTATTTAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1836
QY 1261 CCTAGTCACAGAATTTCAGGACTGTCTCCTCCAGGACCAAGTGGC 1306
Db |||||||
1837 CCTAGTCACAGAATTTCAGGACTGTCTCCTCCAGGACCAAGTGGC 1882

RESULT 8

AAS29737

ID AAS29737 standard; DNA; 2046 BP.

XX

AC AAS29737;

XX

DT 21-NOV-2001 (first entry)

XX

DE Human endocrine polypeptide encoding genomic DNA SEQ ID No 463.

XX

KW Endocrine protein; human; mouse; rabbit; goat; horse; food additive; cat;
KW dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
KW antirheumatic; antiproliferative; cytostatic; cardiac; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
KW ophthalmological; vulnery; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;

wound healing; skin aging; organ transplantation; food preservative;
tissue regeneration; anti-infertility.

Homo sapiens.

WO200155364-A2.

02-AUG-2001.

17-JAN-2001; 2001WO-US001308.

31-JAN-2000; 2000US-0179065P.

04-FEB-2000; 2000US-0180628P.

24-FEB-2000; 2000US-0184664P.

02-MAR-2000; 2000US-0186350P.

16-MAR-2000; 2000US-0189874P.

17-MAR-2000; 2000US-0190076P.

18-APR-2000; 2000US-0198123P.

19-MAY-2000; 2000US-0205515P.

07-JUN-2000; 2000US-0209467P.

28-JUN-2000; 2000US-0214886P.

30-JUN-2000; 2000US-0215135P.

07-JUL-2000; 2000US-0216647P.

07-JUL-2000; 2000US-0216880P.

11-JUL-2000; 2000US-0217487P.

11-JUL-2000; 2000US-0217496P.

14-JUL-2000; 2000US-0218290P.

26-JUL-2000; 2000US-0220963P.

26-JUL-2000; 2000US-0220964P.

14-AUG-2000; 2000US-0224518P.

14-AUG-2000; 2000US-0224519P.

14-AUG-2000; 2000US-0225213P.

14-AUG-2000; 2000US-0225214P.

14-AUG-2000; 2000US-0225266P.

14-AUG-2000; 2000US-0225267P.

14-AUG-2000; 2000US-0225268P.

14-AUG-2000; 2000US-0225270P.

14-AUG-2000; 2000US-0225447P.

14-AUG-2000; 2000US-0225757P.

14-AUG-2000; 2000US-0225758P.

14-AUG-2000; 2000US-0225759P.

18-AUG-2000; 2000US-0226279P.

22-AUG-2000; 2000US-0226681P.

22-AUG-2000; 2000US-0226868P.

22-AUG-2000; 2000US-0227182P.

23-AUG-2000; 2000US-0227009P.

30-AUG-2000; 2000US-0228924P.

01-SEP-2000; 2000US-0229287P.

01-SEP-2000; 2000US-0229343P.

01-SEP-2000; 2000US-0229344P.

01-SEP-2000; 2000US-0229345P.

05-SEP-2000; 2000US-0229509P.

05-SEP-2000; 2000US-0229513P.

06-SEP-2000; 2000US-0230437P.

06-SEP-2000; 2000US-0230438P.

08-SEP-2000; 2000US-0231242P.

08-SEP-2000; 2000US-0231243P.

08-SEP-2000; 2000US-0231244P.

08-SEP-2000; 2000US-0231413P.

08-SEP-2000; 2000US-0231414P.

08-SEP-2000; 2000US-0232080P.

08-SEP-2000; 2000US-0232081P.

12-SEP-2000; 2000US-0231968P.

14-SEP-2000; 2000US-0232397P.

14-SEP-2000; 2000US-0232398P.

14-SEP-2000; 2000US-0232399P.

14-SEP-2000; 2000US-0232400P.

14-SEP-2000; 2000US-0232401P.

14-SEP-2000; 2000US-0233063P.

14-SEP-2000; 2000US-0233064P.

14-SEP-2000; 2000US-0233065P.

21-SEP-2000; 2000US-0234223P.

21-SEP-2000; 2000US-0234274P.

QY 481 CTGGTGAGCAGCCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTTATATC 540
Db |||||
QY 1057 CTGGTGAGCAGCCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTTATATC 1116
Db |||||
QY 541 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGCTTACACCAAC 600
Db |||||
QY 1117 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGCTTACACCAAC 1176
QY 601 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 660
Db |||||
QY 1177 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 1236
QY 661 ATCCACCGCCAGGTCACAAAGAGCAGCAGGCACTGGACCAATACAAAGTTGGCAGGCA 720
Db |||||
QY 1237 ATCCACCGCCAGGTCACAAAGAGCAGCAGGCACTGGACCAATACAAAGTTGGCAGGCA 1296
QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGTTCCAGGAG 780
Db |||||
QY 1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGTTCCAGGAG 1356
QY 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTCAAGAGGAGTTTCTATCTGAGCCAGTCAGT 840
Db |||||
QY 1357 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTCAAGAGGAGTTTCTATCTGAGCCAGTCAGT 1416
QY 841 GCTGCCACACCCAGACCCCTGGAAAGGGGACTCATCAGAAAGTGGGAGACCCAGATCAACAGC 900
Db |||||
QY 1417 GCTGCCACACCCAGACCCCTGGAAAGGGGACTCATCAGAAAGTGGGAGACCCAGATCAACAGC 1476
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 960
Db |||||
QY 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 1536
QY 961 ATTAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGTGAATCAATG 1020
Db |||||
QY 1537 ATTAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGTGAATCAATG 1596
QY 1021 TGTGTTGCTGTGTTCTCTGCTTTCCTGCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1080
Db |||||
QY 1597 TGTGTTGCTGTGTTCTCTGCTTTCCTGCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1656
QY 1081 CTGGATGCGAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCTCAACATT 1140
Db |||||
QY 1657 CTGGATGCGAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCTCAACATT 1716
QY 1141 CTCAATGTTGCTCATCAACCTGCTGCTTATGCGAGCCATGAACCGCAATTCGCGCAAGCA 1200
Db |||||
QY 1717 CTCAATGTTGCTCATCAACCTGCTGCTTATGCGAGCCATGAACCGCAATTCGCGCAAGCA 1776
QY 1201 TATGGTCCATTTTAAAGAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAGACTGTGAC 1260
Db |||||
QY 1777 TATGGTCCATTTTAAAGAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAGACTGTGAC 1836
QY 1261 CCTAGTACCCAGAAATTCAGGAGTGTCTCCTCCAGGACCAAAAGTGGC 1306
Db |||||
QY 1837 CCTAGTACCCAGAAATTCAGGAGTGTCTCCTCCAGGACCAAAAGTGGC 1882

RESULT 9

ABT07831

ID ABT07831 standard; DNA; 2046 BP.

XX AC ABT07831;

XX DT 14-NOV-2002 (first entry)

XX DE Novel human nucleic acid SEQ ID No 130.

XX KW Immunostimulant; antirheumatic; antiarthritic; neuroprotective;

XX KW antiallergic; antidiabetic; antiasthmatic; antiinflammatory; nootropic;

XX KW immunosuppressive; anticoagulant; thrombolytic; antiatherosclerotic;

XX KW cytostatic; nephrotropic; antiparkinsonian; gynecological; virucide;

XX KW antibacterial; antiarrhythmic; fungicide; HCFAT05; HWAEE95; HTNEM01;

KW immunodeficiency; autoimmune disorder; allergic reaction; cardiovascular;
KW inflammatory condition; graft-versus-host disease; reproductive system;
KW blood-related disorder; hyperproliferative; endocrine; neurological;
KW respiratory; renal; infectious disease; gastrointestinal; gene therapy;
KW neuronal growth; neuronal disorder; neuro-degenerative condition;
KW keratinocyte growth; human; ds.

XX Homo sapiens.

XX US2002086330-A1.

XX PD 04-JUL-2002.

XX PF 17-JAN-2001; 2001US-00764893.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 07-JUL-2000; 2000US-0216647P.

XX PR 07-JUL-2000; 2000US-0216880P.

XX PR 11-JUL-2000; 2000US-0217487P.

XX PR 11-JUL-2000; 2000US-0217496P.

XX PR 14-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

XX PR 26-JUL-2000; 2000US-0220964P.

XX PR 14-AUG-2000; 2000US-0224518P.

XX PR 14-AUG-2000; 2000US-0224519P.

XX PR 14-AUG-2000; 2000US-0225267P.

XX PR 14-AUG-2000; 2000US-0225268P.

XX PR 14-AUG-2000; 2000US-0225270P.

XX PR 14-AUG-2000; 2000US-0225447P.

XX PR 14-AUG-2000; 2000US-0225757P.

XX PR 14-AUG-2000; 2000US-0225758P.

XX PR 22-AUG-2000; 2000US-0226868P.

XX PR 30-AUG-2000; 2000US-0228924P.

XX PR 01-SEP-2000; 2000US-0229287P.

XX PR 01-SEP-2000; 2000US-0229343P.

XX PR 01-SEP-2000; 2000US-0229344P.

XX PR 01-SEP-2000; 2000US-0229345P.

XX PR 05-SEP-2000; 2000US-0229509P.

XX PR 05-SEP-2000; 2000US-0229513P.

XX PR 08-SEP-2000; 2000US-0231413P.

XX PR 21-SEP-2000; 2000US-0234223P.

XX PR 21-SEP-2000; 2000US-0234274P.

XX PR 25-SEP-2000; 2000US-0234997P.

XX PR 27-SEP-2000; 2000US-0235834P.

XX PR 29-SEP-2000; 2000US-0236327P.

XX PR 29-SEP-2000; 2000US-0236367P.

XX PR 29-SEP-2000; 2000US-0236368P.

XX PR 29-SEP-2000; 2000US-0236369P.

XX PR 29-SEP-2000; 2000US-0236370P.

XX PR 02-OCT-2000; 2000US-0236802P.

XX PR 02-OCT-2000; 2000US-0237037P.

XX PR 02-OCT-2000; 2000US-0237038P.

XX PR 02-OCT-2000; 2000US-0237039P.

XX PR 02-OCT-2000; 2000US-0237040P.

XX PR 13-OCT-2000; 2000US-0239935P.

XX PR 20-OCT-2000; 2000US-0240960P.

XX PR 20-OCT-2000; 2000US-0241785P.

XX PR 20-OCT-2000; 2000US-0241809P.

XX PR 01-NOV-2000; 2000US-0244617P.

XX PR 17-NOV-2000; 2000US-0249299P.

XX PR 08-DEC-2000; 2000US-0251856P.

XX PR 08-DEC-2000; 2000US-0251868P.

XX PR 08-DEC-2000; 2000US-0251869P.

XX PA (ROSE/) ROSEN C A.

XX PA (RUBE/) RUBEN S M.

XX PA (BARA/) BARASH S C.

XX PI Rosen CA, Ruben SM, Barash SC;

XX WPI; 2002-665432/71.

Db 1237 ATCCACGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATAACAAGTTGCGACAGGCA 1296
QY 721 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCCTGGTCGTTTCCAGGAG 780
Db 1297 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCCTGGTCGTTTCCAGGAG 1356
QY 781 CTGGACAGCAGGTTTAGCATCAGAGGACCCAGTGGAGGGAATTCATCTGAGCCACTCAGT 840
Db 1357 CTGGACAGCAGGTTTAGCATCAGAGGACCCAGTGGAGGGAATTCATCTGAGCCACTCAGT 1416
QY 841 GCTGCCACCAACCCAGACCCCTGGAGGGGACTCATCAGAACTGGGAGACCAGATCAACAGC 900
Db 1417 GCTGCCACCAACCCAGACCCCTGGAGGGGACTCATCAGAACTGGGAGACCAGATCAACAGC 1476
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCCA 960
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCCA 1536
QY 961 ATTAAGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
Db 1537 ATTAAGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
QY 1021 TGTTTTGTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGCTGCTCAACATT 1080
Db 1597 TGTTTTGTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGCTGCTCAACATT 1656
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACCTGG 1140
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACCTGG 1716
QY 1141 CTCAATGTTGTCATCAACCCCTGTGCTATGCAGCCATGAACCGCCCAATTCCGCCCAAGCA 1200
Db 1717 CTCAATGTTGTCATCAACCCCTGTGCTATGCAGCCATGAACCGCCCAATTCCGCCCAAGCA 1776
QY 1201 TATGGCTCCATTTAAAAAGAGGGCCCGGAGTTTCCATAGGTCCTCATTAGAACTGTGAC 1260
Db 1777 TATGGCTCCATTTAAAAAGAGGGCCCGGAGTTTCCATAGGTCCTCATTAGAACTGTGAC 1836
QY 1261 CCTAGTCACAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1306
Db 1837 CCTAGTCACAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1882

RESULT 11

ACD01492
ID ACD01492 standard; DNA; 2046 BP.

XX AC ACD01492;

XX DT 30-JUL-2003 (first entry)

XX DE Human genomic DNA #1.

XX KW Human; gene; ds; kidney disorder; cardiovascular disorder; arrhythmia;
KW glomerulonephritis; urinary tract infection; chronic nephritis; anaemia;
KW carcinoïd heart disease; endocarditis; blood disorder; thrombosis;
KW haemoglobin abnormality; electrolyte imbalance; neoplastic disorder;
KW cancer; respiratory disorder; acute rhinitis; sinusitis; pharyngitis;
KW neurological disorder; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease.

XX OS Homo sapiens.

XX PN US2003013649-A1.

XX PD 16-JAN-2003.

XX PF 21-NOV-2001; 2001US-00989442.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 02-OCT-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.

QY	661	ATCCACCGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGCGACAGGCA	720
Db	1237	ATCCACCGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGCGACAGGCA	1296
QY	721	AGCATCCACTCCAAACCATGTGGCCAGGACTGATAGGCGCATGCCTGGTCTGTTCCAGGAG	780
Db	1297	AGCATCCACTCCAAACCATGTGGCCAGGACTGATAGGCGCATGCCTGGTCTGTTCCAGGAG	1356
QY	781	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT	840
Db	1357	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT	1416
QY	841	GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC	900
Db	1417	GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC	1476
QY	901	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGGCCA	960
Db	1477	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGGCCA	1536
QY	961	ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	1020
Db	1537	ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	1596
QY	1021	TGTTTTGCTGTGTTCCCTCTGCTTTTGCCCTGAGCTACATCCCCTTCTTGCTGCTCAACATT	1080
Db	1597	TGTTTTGCTGTGTTCCCTCTGCTTTTGCCCTGAGCTACATCCCCTTCTTGCTGCTCAACATT	1656
QY	1081	CTGGATGCCAGAGTCCAGGCTCCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACCTGG	1140
Db	1657	CTGGATGCCAGAGTCCAGGCTCCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACCTGG	1716
QY	1141	CTCAATGGTTGCATCAACCCCTGTGCTCTATGACGCCATGAACCGCCAATTCGCGCAAGCA	1200
Db	1717	CTCAATGGTTGCATCAACCCCTGTGCTCTATGACGCCATGAACCGCCAATTCGCGCAAGCA	1776
QY	1201	TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC	1260
Db	1777	TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC	1836
QY	1261	CCTAGTCACCAAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC	1306
Db	1837	CCTAGTCACCAAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC	1882

RESULT 12

ADC46506
ID ADC46506 standard; DNA; 2046 BP.

XX
AC ADC46506;

XX
DT 18-DEC-2003 (first entry)

XX
DE Human neoplastic disease-a

XX Neoplastic disease-associated polypeptide; gene the

KW hyperproliferative disease; cancer; autoimmune disorder; diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KW autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder;
KW haematologic disorder; anaemia; thrombocytopaenia; allergic reaction;
KW asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury;
KW inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; renal disorder;
KW acute glomerulonephritis; end-stage renal disease;
KW cardiovascular disorder; atherosclerosis; myocarditis;
KW infectious disease; AIDS; cachexia; anorexia; wound healing;
KW epithelial cell proliferation; Human; ds.

XX
OS Homo sapiens.

XX
PN US2003082758-A1.

XX
PD 01-MAY-2003.

PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764854.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Ruben SM, Barash SC;
XX WPI; 2003-786918/74.

XX New isolated human neoplastic disease-associated polypeptides and
PT polynucleotides, useful for diagnosing, preventing, prognosticating or
PT treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
PT disease.
XX Disclosure; SEQ ID NO 592; 302pp; English.
XX The invention relates to one of 238 disclosed human neoplastic disease-
CC associated polypeptides encoded by 171 disclosed cDNA sequences
CC (including their domains, epitopes, full-length proteins, allelic variants
CC or species homologues). Also included are there encoding nucleic acids, a
CC recombinant vector comprising the nucleic acid, a recombinant host cell
CC comprising the nucleic acid (expressing the protein), an isolated
CC antibody that binds specifically to the isolated polypeptide, preventing,
CC treating or ameliorating a medical condition, diagnosing a pathological
CC condition or a susceptibility to a pathological condition in a subject,
CC identifying a binding partner to the polypeptide, identifying an activity
CC in a biological assay, and the gene corresponding to the cDNA sequence.
CC The polypeptides, polynucleotides and antibodies are useful for
CC detecting, preventing, diagnosing, prognosticating, treating or
CC ameliorating medical conditions such as hyperproliferative diseases or
CC cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
CC systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
CC or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
CC anaemia or thrombocytopaenia), allergic reactions including asthma or
CC eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
CC inflammatory bowel disease or Crohn's disease), neurodegenerative

Query Match 99.6%; Score 1306; DB 9; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATGCTAGGTTCTGATTCCTCTTCTCTTCCACCTCTGCTCTTTAGCCTCTATC 60
Db |||||
577 TTGAATGCTAGGTTCTGATTCCTCTTCTCTTCCACCTCTGCTCTTTAGCCTCTATC 636
QY 61 ATGTGGACAGCTCTGACGCCCACTTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 120
Db |||||
637 ATGTGGACAGCTCTGACGCCCACTTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 696
QY 121 TATGTTGAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 180
Db |||||
697 TATGTTGAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 756
QY 181 ACCCTACTGGCCTTGGCCATCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
Db |||||
757 ACCCTACTGGCCTTGGCCATCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
QY 241 AACCTACACTGGCTGATCTCTCTACTGACAGCTCCCTCAGCCCTTCTCTGTGGACACC 300
Db |||||
817 AACCTACACTGGCTGATCTCTCTACTGACAGCTCCCTCAGCCCTTCTCTGTGGACACC 876
QY 301 TACCTCCACTGCACCTGGCGACCGGTGCCACCTTCTGAGGGGTATTTGGGCTCCCTCTT 360
Db |||||
877 TACCTCCACTGCACCTGGCGACCGGTGCCACCTTCTGAGGGGTATTTGGGCTCCCTCTT 936
QY 361 TTGCTCCCAATTCTGTCTCCATCTGACCCCTCTGCTCATGCGACTGGGACGCTACCTC 420
Db |||||
937 TTGCTCCCAATTCTGTCTCCATCTGACCCCTCTGCTCATGCGACTGGGACGCTACCTC 996
QY 421 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 480
Db |||||
997 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 1056
QY 481 CTGGTGAGCACCTGGGTTGTGGGGTGGCCAGCTTTTGCTCCCTCTGGCCCTATTTATATC 540
Db |||||
1057 CTGGTGAGCACCTGGGTTGTGGGGTGGCCAGCTTTTGCTCCCTCTGGCCCTATTTATATC 1116
QY 541 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGCGCGCTTACACACC 600
Db |||||
1117 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGCGCGCTTACACACC 1176


```
QY 601 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 660
    |||
Db 1177 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 1236

QY 661 ATCCACCGCCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 720
    |||
Db 1237 ATCCACCGCCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 1296

QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTGTTCCAGGAG 780
    |||
Db 1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTGTTCCAGGAG 1356

QY 781 CTGGACAGCAGGTTAGCATCAGAGGAGACCCAGTGTAGGGGATTTTCATCTGAGCCAGTCAGT 840
    |||
Db 1357 CTGGACAGCAGGTTAGCATCAGAGGAGACCCAGTGTAGGGGATTTTCATCTGAGCCAGTCAGT 1416

QY 841 GCTGCCACACCCAGACCCCTGTGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 900
    |||
Db 1417 GCTGCCACACCCAGACCCCTGTGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 1476

QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGATCTGCCAAAGCCCAAGCCA 960
    |||
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGATCTGCCAAAGCCCAAGCCA 1536

QY 961 ATTAAGAGCCAGAAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
    |||
Db 1537 ATTAAGAGCCAGAAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596

QY 1021 TGTTTTGTGCTGTCTCCTCTGCTTTGCCCTGAGCTACATCCCTCTTTGCTGCTCAACATT 1080
    |||
Db 1597 TGTTTTGTGCTGTCTCCTCTGCTTTGCCCTGAGCTACATCCCTCTTTGCTGCTCAACATT 1656

QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGTTGGTCCACATGCTTGTGCCAACCTCACCTGG 1140
    |||
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGTTGGTCCACATGCTTGTGCCAACCTCACCTGG 1716

QY 1141 CTCAATGGTTGCATCAACCCCTGTGCTCTATGCAGCCATGAACCGCCAATTCGGCCCAAGCA 1200
    |||
Db 1717 CTCAATGGTTGCATCAACCCCTGTGCTCTATGCAGCCATGAACCGCCAATTCGGCCCAAGCA 1776

QY 1201 TATGGCTCCATTTTAAAGAGAGGGCCCGGAGTTTCCATAGGTTCCATTAGAACTGTGAC 1260
    |||
Db 1777 TATGGCTCCATTTTAAAGAGAGGGCCCGGAGTTTCCATAGGTTCCATTAGAACTGTGAC 1836

QY 1261 CCTAGTCACAGAAATTCAGGACTGTCTCTCTCCAGGACCAAAAGTGGC 1306
    |||
Db 1837 CCTAGTCACAGAAATTCAGGACTGTCTCTCTCCAGGACCAAAAGTGGC 1882
```

```
RESULT 13
AAI68792
ID AAI68792 standard; DNA; 5460 BP.
XX
AC AAI68792;
XX
DE 22-JAN-2002 (first entry)
XX
FH Key Location/Qualifiers
DE CDS 1663..2853
FT /*tag= a
FT /product= "MAR1"
FT polyA_signal 3049..3053
FT /*tag= b
FT polyA_signal 3461..3465
FT /*tag= c
FT polyA_signal 5184..5188

OS Homo sapiens.
XX
KW MAR1; monoamine receptor-1; human; cytostatic; gene therapy; tumour;
KW psychiatric disorder; transgenic animal; knockout animal; ds.
XX
XX
```

```
FT /*tag= d
XX DE10021474-A1.
XX
PD 08-NOV-2001.
XX
PF 03-MAY-2000; 2000DE-01021474.
XX
PR 03-MAY-2000; 2000DE-01021474.
XX
PA (BRUE/) BRUESS M.
PA (BOEN/) BOENISCH H.
XX
PI Bruess M, Boenisch H;
XX
XX WPI; 2002-011956/02.
XX
DR P-PSDB; AAG80225.
XX
PT New monoamine receptor-1 gene, MAR1, useful for diagnosis and treatment
PT of MAR1-related diseases.
XX
PS Disclosure; Page 3-4; 6pp; German.
XX
CC This invention describes a novel human monoamine receptor-1 (MAR1) gene
CC (I) which has cytostatic activity and can be used for gene therapy. (I),
CC and derived (anti)sense oligonucleotides, are useful in treatment and
CC diagnosis of (I)-related diseases (possibly tumours and psychiatric
CC disorders), for producing transgenic/knockout animals, and for
CC recombinant expression of the protein (II) that it encodes. (II) is
CC useful in ligand-binding studies and screening assays, also for treatment
CC and diagnosis of (II)-related diseases. This sequence encodes the human
CC MAR1 monoamine receptor-1 protein
XX
SQ Sequence 5460 BP; 1603 A; 1167 C; 1268 G; 1422 T; 0 U; 0 Other;

Query Match 99.6%; Score 1306; DB 6; Length 5460;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATGCTAGGTTCTGATTCCCTCTTCCCTCTTCCACCCCTCTGCCTCTTTAGCCTCTATC 60
    |||
Db 1603 TTGAATGCTAGGTTCTGATTCCCTCTTCCCTCTTCCACCCCTCTGCCTCTTTAGCCTCTATC 1662

QY 61 ATGTGGAACAGCTCTGACGGCCAACTTCTCCTGTACTACCATGAGTCTGTGTGGGCTATCGT 120
    |||
Db 1663 ATGTGGAACAGCTCTGACGGCCAACTTCTCCTGTACTACCATGAGTCTGTGTGGGCTATCGT 1722

QY 121 TATGTTGCAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 180
    |||
Db 1723 TATGTTGCAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 1782

QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
    |||
Db 1783 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 1842

QY 241 AACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACACC 300
    |||
Db 1843 AACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACACC 1902

QY 301 TACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 360
    |||
Db 1903 TACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 1962

QY 361 TTTGCCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 420
    |||
Db 1963 TTTGCCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 2022

QY 421 CTCATTGCCCAACCCCTAAGCTTTTCCCAAGTTTTCAGTGCACCAAGGGGATAGTGTGGCA 480
    |||
Db 2023 CTCATTGCCCAACCCCTAAGCTTTTCCCAAGTTTTCAGTGCACCAAGGGGATAGTGTGGCA 2082

QY 481 CTGGTGAGCACCTGGGTTGTGGCGGTGGCCAGCTTTGCTCCCTCTGCTCCCTATTATATC 540
    |||
```

Db 2083 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 2142
QY 541 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGGCGGCGCTTACACCACC 600
Db 2143 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGGCGGCGCTTACACCACC 2202
QY 601 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 660
Db 2203 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 2262
QY 661 ATCCACCGCCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 720
Db 2263 ATCCACCGCCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 2322
QY 721 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCCTGGTCTGTTCCAGGAG 780
Db 2323 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCCTGGTCTGTTCCAGGAG 2382
QY 781 CTGGACAGCAGGTAGCATCAGGAGGACCCAGTGGGGATTTCATCTGAGCCAGTCAGT 840
Db 2383 CTGGACAGCAGGTAGCATCAGGAGGACCCAGTGGGGATTTCATCTGAGCCAGTCAGT 2442
QY 841 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGAGACCAGATCAACAGC 900
Db 2443 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGAGACCAGATCAACAGC 2502
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGGCA 960
Db 2503 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGGCA 2562
QY 961 ATTAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGTGACTCGAATG 1020
Db 2563 ATTAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGTGACTCGAATG 2622
QY 1021 TGTGTTGCTGTCTCTCTGCTTTGCCCTGAGCTACATCCCTCTCTTGTGCTGCTCAACATT 1080
Db 2623 TGTGTTGCTGTCTCTCTGCTTTGCCCTGAGCTACATCCCTCTCTTGTGCTGCTCAACATT 2682
QY 1081 CTGGATGCCAGATCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCACTGG 1140
Db 2683 CTGGATGCCAGATCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCACTGG 2742
QY 1141 CTCAATGTTGTCATCAACCTGTGCTCTATGCAGCCATGAACGCCCAATTCCGCCAAGCA 1200
Db 2743 CTCAATGTTGTCATCAACCTGTGCTCTATGCAGCCATGAACGCCCAATTCCGCCAAGCA 2802
QY 1201 TATGGCTCCATTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1260
Db 2803 TATGGCTCCATTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 2862
QY 1261 CCTAGTCACAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1306
Db 2863 CCTAGTCACAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 2908

RESULT 14

AAV38513
ID AAV38513 standard; cDNA; 1498 BP.

XX AAV38513;

AC AAV38513;

XX 07-OCT-1998 (first entry)

DE Human 7-transmembrane receptor encoding cDNA clone HNFJD15.

XX G-protein coupled receptor; HNFJD15; treatment; diagnosis; infection;

KW HIV-1; HIV-2; cancer; screening; human; 7-transmembrane receptor;

KW Parkinson's disease; vaccine; ss.

XX Homo sapiens.

OS

FT FT /*tag= a
XX FT /product= "human 7-transmembrane receptor, HNFJD15"
PN EP853125-A2.
XX 15-JUL-1998.
XX 20-NOV-1997; 97EP-00309347.
XX 09-JAN-1997; 97US-00775428.
XX (SMIK) SMITHKLINE BEECHAM CORP.
PI Sathe GM, Fuetterer WS, Bergsma DJ, Ellis C;
XX WPI; 1998-364650/32.
DR P-PSDB; AAW62598.
XX Human G-protein coupled receptor, HNFJD15 - used e.g. in treatment and
PT diagnosis of infections e.g. by HIV-1, HIV-2 and cancers and screening of
PT antagonistic or agonistic compounds.
XX Claim 4; Fig 1; 19pp; English.
PS This cDNA encodes a human 7-transmembrane receptor, HNFJD15. HNFJD15 is a
XX human G-protein coupled receptor and are used in vaccines to protect
CC mammals from infections e.g. bacterial, fungal, protozoan and viral
CC infections (especially infections caused by HIV-1 or HIV-2), cancers and
CC Parkinson's disease. The HNFJD15 polypeptides can be used to produce
CC antibodies which are used to treat such infections, isolate or identify
CC clones expressing the polypeptide or to purify the polypeptide. The
CC polypeptides can also be used to screen for compounds binding to,
CC activating or inhibiting activation of HNFJD15. They can be used to
CC diagnose diseases and susceptibility to diseases related to expression or
CC activity of HNFJD15
XX
SQ Sequence 1498 BP; 346 A; 438 C; 349 G; 365 T; 0 U; 0 Other;

Query Match 95.8%; Score 1256.4; DB 2; Length 1498;
Best Local Similarity 99.9%; Pred.No. 0;
Matches 1257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 TTAGCCTCTATCATGTGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG 108
Db 64 TCAGCCTCTATCATGTGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG 123
QY 109 CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGCACCGTG 168
Db 124 CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGCACCGTG 183
QY 169 GGCAATGTGCTCACCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAAC 228
Db 184 GGCAATGTGCTCACCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAAC 243
QY 229 CTGCTCATAGCCAAACCTCACACTGGCTGATCTCTCTACTGACGCTCTCTTACGCCCTTC 288
Db 244 CTGCTCATAGCCAAACCTCACACTGGCTGATCTCTCTACTGACGCTCTCTTACGCCCTTC 303
QY 289 TCTGTGGACACCTACCTCCACCTTGGCACTGGCGCACCCGGTGGCCACTTCTGACGGGTATT 348
Db 304 TCTGTGGACACCTACCTCCACCTTGGCACTGGCGCACCCGGTGGCCACTTCTGACGGGTATT 363
QY 349 GGGCTCCTCTTTTGGCTCCCAATTTCTGCTCTCCATCTCTGACGCTCTCTTACGCCCTTC 408
Db 364 GGGCTCCTCTTTTGGCTCCCAATTTCTGCTCTCCATCTCTGACGCTCTCTTACGCCCTTC 423
QY 409 GGACGCTACCTCCTCATTTGCCCACTTAAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGG 468
Db 424 GGACGCTACCTCCTCATTTGCCCACTTAAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGG 483
QY 469 ATAGTGTGGCACTGGTGAGCACCTGGGTTGTGGGGCTGGCCAGCTTTGCTCCCTCTGG 528
Db 484 ATAGTGTGGCACTGGTGAGCACCTGGGTTGTGGGGCTGGCCAGCTTTGCTCCCTCTGG 543

Search completed: September 23, 2004, 23:57:13
Job time : 596.574 secs

QY 229 CTGCTCATAGCAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC 288
Db |||||
259 CTGCTCATAGCAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC 318
QY 289 TCTGTGGACACCTACCTCCACCTGCCTGGCGCACCGGTGCACCTTCTGCGGGTATTT 348
Db |||||
319 TCTGTGGACACCTACCTCCACCTGCCTGGCGCACCGGTGCACCTTCTGCGGGTATTT 378
QY 349 GGGCTCCTCTCTTTTGGCTCCCAATTCTGTCTCCATCCTGACCTCTGCCTCATCGCACTG 408
Db |||||
379 GGGCTCCTCTCTTTTGGCTCCCAATTCTGTCTCCATCCTGACCTCTGCCTCATCGCACTG 438
QY 409 GGACGCTACCTCCTCATTTGCCCCACCCCTAAGCTTTTTCCTCCCAAGTTTTCAGTGCCCAAGGGG 468
Db |||||
439 GGACGCTACCTCCTCATTTGCCCCACCCCTAAGCTTTTTCCTCCCAAGTTTTCAGTGCCCAAGGGG 498
QY 469 ATAGTGTGGCACTGGTGAGCACCTGGGTGTGGGGCGTGGCGCAGCTTTGCTCCCTCTCTGG 528
Db |||||
499 ATAGTGTGGCACTGGTGAGCACCTGGGTGTGGGGCGTGGCGCAGCTTTGCTCCCTCTCTGG 558
QY 529 CCTATTATATCCTGGTACCTGATGCTGCACCTGACCTTTGACCGCATCCGAGGCCGG 588
Db |||||
559 CCTATTATATCCTGGTACCTGATGCTGCACCTGACCTTTGACCGCATCCGAGGCCGG 618
QY 589 CTTTACACCACTCCTCATGGGCACTCTATTGCTGGCTCAGCAGTGTGGCATC 648
Db |||||
619 CTTTACACCACTCCTCATGGGCACTCTATTGCTGGCTCAGCAGTGTGGCATC 678
QY 649 TTCTATTGCTCATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAG 708
Db |||||
679 TTCTATTGCTCATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAG 738
QY 709 TTGCGACAGGCAAGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT 768
Db |||||
739 TTGCGACAGGCAAGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT 798
QY 769 CGTTTCCAGGAGCTGGACAGCAGGTAGCATCAGGAGGACCCAGTGGGGATTTCATCT 828
Db |||||
799 CGTTTCCAGGAGCTGGACAGCAGGTAGCATCAGGAGGACCCAGTGGGGATTTCATCT 858
QY 829 GAGCCAGTCACTGCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGAC 888
Db |||||
859 GAGCCAGTCACTGCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGAC 918
QY 889 CAGATCAACACAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCC 948
Db |||||
919 CAGATCAACAGAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCC 978
QY 949 AAAGCCCAAGCAATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAG 1008
Db |||||
979 AAAGCCCAAGCAATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAG 1038
QY 1009 GTGACTCGAATGTGTTTTGCTGTGTCTCCTCTGCTTTGCCCTGAGCTACATCCCTCTCTTG 1068
Db |||||
1039 GTGACTCGAATGTGTTTTGCTGTGTCTCCTCTGCTTTGCCCTGAGCTACATCCCTCTCTTG 1098
QY 1069 CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTCTGCC 1128
Db |||||
1099 CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTCTGCC 1158
QY 1129 AACCTCACTGGCTCAATGGTTGCAATCAACCCCTGTCTATGCAGCCCATGAACCGCCAA 1188
Db |||||
1159 AACCTCACTGGCTCAATGGTTGCAATCAACCCCTGTCTATGCAGCCCATGAACCGCCAA 1218
QY 1189 TTCCGCCAAGCATATGGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCAT 1248
Db |||||
1219 TTCCGCCAAGCATATGGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCAT 1278
QY 1249 TAGAACTGTGACCCCTAGTCACCAAGATTTCAGGACTGTCTCTCCAGGACCAAGTGGC 1306
Db |||||
1279 TAGAACTGTGACCCCTAGTCACCAAGATTTCAGGACTGTCTCTCCAGGACCAAGTGGC 1336

GenCore version 5.1.6
Copyright (c) 1993 - 2004 , Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2004, 02:47:20 ; Search time 1055.3 Seconds
(without alignments)
6292.206 Million cell updates/sec

Title: US-10-029-436-1
Perfect score: 1311
Sequence: 1 ttgaatgctagttcttgatt.....caggaccaagtggcaggtta 1311

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3337386 seqs, 2532474682 residues

Total number of hits satisfying chosen parameters: 6674772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length DB ID	Description
1	1311	100.0	1311 15	US-10-029-436-1 Sequence 1, Appli
2	1306	99.6	2046 9	US-09-764-853-875 Sequence 875, App
3	1306	99.6	2046 10	US-09-989-442-155 Sequence 155, App
c 4	1306	99.6	2046 10	US-09-764-886-84 Sequence 84, Appl
5	1306	99.6	2046 11	US-09-764-875-1209 Sequence 1209, Ap
c 6	1306	99.6	2046 13	US-09-764-886-84 Sequence 84, Appl
7	1306	99.6	2046 13	US-09-764-893-130 Sequence 130, App
8	1306	99.6	2046 15	US-10-073-865-130 Sequence 130, App
9	1306	99.6	2046 15	US-10-103-313-592 Sequence 592, App
10	1256.4	95.8	1498 9	US-09-826-508-37 Sequence 37, Appl
11	1256.4	95.8	1546 15	US-10-225-567A-584 Sequence 584, App
12	1256.4	95.8	1595 9	US-09-798-710-1 Sequence 1, Appli
13	1255.6	95.8	1579 15	US-10-073-885-11 Sequence 11, Appl
14	1191	90.8	1191 13	US-10-343-650A-45 Sequence 45, Appl

15	1188	90.6	1188	15	US-10-094-417-3	Sequence 3, Appli
16	887.6	67.7	1191	15	US-10-094-417-21	Sequence 21, Appl
17	754	57.5	1333	15	US-10-017-161-1921	Sequence 1921, Ap
c 18	525	40.0	525	15	US-10-029-386-12527	Sequence 12527, A
19	360.4	27.5	485	16	US-10-264-237-348	Sequence 348, App
20	355	27.1	483	9	US-09-764-853-62	Sequence 62, Appl
21	355	27.1	483	10	US-09-989-442-13	Sequence 13, Appl
22	355	27.1	483	10	US-09-764-886-26	Sequence 26, Appl
23	355	27.1	483	11	US-09-764-875-43	Sequence 43, Appl
24	355	27.1	483	13	US-09-764-886-26	Sequence 26, Appl
25	355	27.1	483	13	US-09-764-893-14	Sequence 14, Appl
26	355	27.1	483	15	US-10-073-865-14	Sequence 14, Appl
27	355	27.1	483	15	US-10-103-313-26	Sequence 26, Appl
28	355	27.1	483	15	US-10-073-885-38	Sequence 38, Appl
c 29	209	15.9	209	15	US-10-029-386-26227	Sequence 26227, A
30	133.6	10.2	494	9	US-09-783-590-6339	Sequence 6339, Ap
31	87.8	6.7	1382	15	US-10-225-567A-419	Sequence 419, App
32	87.8	6.7	1382	17	US-10-293-998-4	Sequence 4, Appli
33	87.8	6.7	1584	16	US-10-305-720-284	Sequence 284, App
34	87.8	6.7	1659	13	US-10-391-074-3	Sequence 3, Appli
35	87	6.6	2481	9	US-09-951-622-1	Sequence 1, Appli
36	87	6.6	2481	15	US-10-325-930-1	Sequence 1, Appli
37	86.2	6.6	1663	9	US-09-961-700A-46	Sequence 46, Appl
38	83	6.3	1738	15	US-10-185-991-3	Sequence 3, Appli
39	83	6.3	1738	15	US-10-238-129-3	Sequence 3, Appli
40	83	6.3	1738	15	US-10-238-667-3	Sequence 3, Appli
41	83	6.3	1738	16	US-10-305-720-1402	Sequence 1402, Ap
42	83	6.3	1786	15	US-10-225-567A-35	Sequence 35, Appl
43	80	6.1	1092	15	US-10-303-204A-15	Sequence 15, Appl
44	80	6.1	3129	15	US-10-303-204A-14	Sequence 14, Appl
45	76.6	5.8	2048	14	US-10-052-589-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-029-436-1
; Sequence 1, Application US/10029436
; Publication No. US20030124138A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E.
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA Encoding A Human Receptor (hp15a) And Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 55180
; CURRENT APPLICATION NUMBER: US/10/029,436
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US/09/179,798A
; PRIOR FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-029-436-1

Query Match	100.0%;	Score 1311;	DB 15;	Length 1311;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1311;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	TTGAATGCTAGTTCTTGATTCCTCTTCTCTTCCACCCCTCTGCCTCTTAGCCTCTATC	60	
Db	1	TTGAATGCTAGTTCTTGATTCCTCTTCTCTTCCACCCCTCTGCCTCTTAGCCTCTATC	60	
Qy	61	ATGTGGAACAGCTCTGACGCCAACTTCTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT	120	
Db	61	ATGTGGAACAGCTCTGACGCCAACTTCTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT	120	
Qy	121	TATGTTGCAGTTAGTGGGGGTGGTGGTGGTGTGACAGGACCCGTGGGCAATGTGCTC	180	
Db	121	TATGTTGCAGTTAGTGGGGGTGGTGGTGGTGTGACAGGACCCGTGGGCAATGTGCTC	180	

QY 181 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
Db 181 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
QY 241 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 300
Db 241 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 300
QY 301 TACCTCCACCTGACCTGGCGCACCGGTGCCACCTTCTGACGGGTATTGGGCTCCTCCTT 360
Db 301 TACCTCCACCTGACCTGGCGCACCGGTGCCACCTTCTGACGGGTATTGGGCTCCTCCTT 360
QY 361 TTTGCCCTCCAATTCTGTCTCCATCTGACCCCTCTGCCTCATCGCACTGGGACGCTACTC 420
Db 361 TTTGCCCTCCAATTCTGTCTCCATCTGACCCCTCTGCCTCATCGCACTGGGACGCTACTC 420
QY 421 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 480
Db 421 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 480
QY 481 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTTGCTCCCTCTGGCCTATTTATATC 540
Db 481 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTTGCTCCCTCTGGCCTATTTATATC 540
QY 541 CTGGTACCTGTAGTCTGACCTGACCTTGACCGCATCCGAGCGCGGCTTACACCACC 600
Db 541 CTGGTACCTGTAGTCTGACCTGACCTTGACCGCATCCGAGCGCGGCTTACACCACC 600
QY 601 ATCCTCATGSGCATCTACTTTGTGCTTGGCTCAGCAGTGTGGCATCTTCTATTGCTC 660
Db 601 ATCCTCATGSGCATCTACTTTGTGCTTGGCTCAGCAGTGTGGCATCTTCTATTGCTC 660
QY 661 ATCCACCGCCAGGTCAACGAGCAGCAGGCACTGGACCCATACAAAGTTGCGACAGGCA 720
Db 661 ATCCACCGCCAGGTCAACGAGCAGCAGGCACTGGACCCATACAAAGTTGCGACAGGCA 720
QY 721 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGTTTCCAGGAG 780
Db 721 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGTTTCCAGGAG 780
QY 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCAGT 840
Db 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCAGT 840
QY 841 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 900
Db 841 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 900
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCTGTGCCAAAGCCAGCCA 960
Db 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCTGTGCCAAAGCCAGCCA 960
QY 961 ATTAAGGAGCCAGAGAGCTCCGGAATTTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
Db 961 ATTAAGGAGCCAGAGAGCTCCGGAATTTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
QY 1021 TGTTTTGCTGTGTTCTCTGCTTTTGGCCTGAGCTACATCCCTTCTTGTCTGCTCAACATT 1080
Db 1021 TGTTTTGCTGTGTTCTCTGCTTTTGGCCTGAGCTACATCCCTTCTTGTCTGCTCAACATT 1080
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGCTGCCAACCTCACTGG 1140
Db 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGCTGCCAACCTCACTGG 1140
QY 1141 CTCAATGGTTGATCAACCCCTGTGCTATGAGCCATGAACCGCCAAATTCGCCCAAGCA 1200
Db 1141 CTCAATGGTTGATCAACCCCTGTGCTATGAGCCATGAACCGCCAAATTCGCCCAAGCA 1200
QY 1201 TATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1260
Db 1201 TATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1260

QY 1261 CCTAGTCACAGAAATTCAGGACTGTCTCTCCAGGACCAAAAGTGGCAGGTA 1311
Db 1261 CCTAGTCACAGAAATTCAGGACTGTCTCTCCAGGACCAAAAGTGGCAGGTA 1311
RESULT 2
US-09-764-853-875
; Sequence 875, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 875
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-875
Query Match 99.6%; Score 1306; DB 9; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGAATGCTAGGTTCTGATTCCCTCTTCTCTCCACCCCTCTGCTCTTTAGCCCTATC 60
Db 577 TTGAATGCTAGGTTCTGATTCCCTCTTCTCTCCACCCCTCTGCTCTTTAGCCCTATC 636
QY 61 ATGTGGACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 120
Db 637 ATGTGGACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 696
QY 121 TATGTTGCACTTAGCTGGGGGTTGGTGGTGTGACAGGACCCGTGGGCAATGTGCTC 180
Db 697 TATGTTGCACTTAGCTGGGGGTTGGTGGTGTGACAGGACCCGTGGGCAATGTGCTC 756
QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
Db 757 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
QY 241 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTTCAGCCCTTCTCTGTGGACACC 300
Db 817 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTTCAGCCCTTCTCTGTGGACACC 876
QY 301 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTCTGCTGCAAGGTATTGGGCTCCTCCTT 360
Db 877 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAAGGTATTGGGCTCCTCCTT 936
QY 361 TTTGCCCTCCAATTCTGTCTCCATCTGACCCCTCTGCTGCAAGGTATTGGGCTCCTCCTT 420
Db 937 TTTGCCCTCCAATTCTGTCTCCATCTGACCCCTCTGCTGCAAGGTATTGGGCTCCTCCTT 996
QY 421 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 480
Db 997 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 1056
QY 481 CTGGTGAGCAGCTGGGTTGTGGCGTGGCCAGCTTTTGCTCCCTCTGGCCTATTTATATC 540
Db 1057 CTGGTGAGCAGCTGGGTTGTGGCGTGGCCAGCTTTTGCTCCCTCTGGCCTATTTATATC 1116
QY 541 CTGGTACCTGTAGTCTGACACCTGACAGCTTTGACCGCATCCGAGCGCGGCTTACACCACC 600
Db 1117 CTGGTACCTGTAGTCTGACACCTGACAGCTTTGACCGCATCCGAGCGCGGCTTACACCACC 1176
QY 601 ATCCTCATGGGCACTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 660
Db 1177 ATCCTCATGGGCACTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 1236
QY 661 ATCCACCGCCAGGTCAACGAGCAGCAGGCACTGGACCAATACAAAGTTGGCAGAGGCA 720

Db 1237 ATCCACCGCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATAACAAGTTGCGACAGGCA 1296
QY 721 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTTCGTTTCCAGGAG 780
Db 1297 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTTCGTTTCCAGGAG 1356
QY 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGAGGGATTTCATCTGAGCCAGTCAGT 840
Db 1357 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGAGGGATTTCATCTGAGCCAGTCAGT 1416
QY 841 GCTGCCACACCCAGACCCCTGGAAAGGGACTCATCAGAAAGTGGAGACCAGATCAACAGC 900
Db 1417 GCTGCCACACCCAGACCCCTGGAAAGGGACTCATCAGAAAGTGGAGACCAGATCAACAGC 1476
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCCAAGCA 960
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCCAAGCA 1536
QY 961 ATTAAGAGACCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
Db 1537 ATTAAGAGACCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
QY 1021 TGTTTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGCTGCTCAACATT 1080
Db 1597 TGTTTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGCTGCTCAACATT 1656
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACCTGG 1140
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACCTGG 1716
QY 1141 CTCAATGGTTCATCAACCCCTGTGCTCTATGCAGCCATGAACGCCCAATTCCGCCAAGCA 1200
Db 1717 CTCAATGGTTCATCAACCCCTGTGCTCTATGCAGCCATGAACGCCCAATTCCGCCAAGCA 1776
QY 1201 TATGGCTCAATTTAAAAAGAGGGCCCGGAGTTTCCATAGGTCCTCATTAGAACTGTGAC 1260
Db 1777 TATGGCTCAATTTAAAAAGAGGGCCCGGAGTTTCCATAGGTCCTCATTAGAACTGTGAC 1836
QY 1261 CCTAGTACCAGAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1306
Db 1837 CCTAGTACCAGAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1882

RESULT 3

US-09-989-442-155
; Sequence 155, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ08
; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02

; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,208
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,245
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414

; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14

Query Match 99.6%; Score 1306; DB 10; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGAATGCTAGGTTCTGATTCCCTCTTCTCTTCCACCCCTGCTGCTCTTTAGCCTCTATC 60
DB 577 TTGAATGCTAGGTTCTGATTCCCTCTTCTCTTCCACCCCTGCTGCTCTTTAGCCTCTATC 636
QY 61 ATGTGGAACAGCTCTGACGCCAAGTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 120
DB 637 ATGTGGAACAGCTCTGACGCCAAGTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 696
QY 121 TATGTTGCAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 180
DB 697 TATGTTGCAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 756
QY 181 ACCCTACTGGCCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
DB 757 ACCCTACTGGCCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
QY 241 AACCTCACACTGGCTGATCTCTCTACTGACAGCTCCCTTACGCCCCCTTCTCTGTGGACACC 300
DB 817 AACCTCACACTGGCTGATCTCTCTACTGACAGCTCCCTTACGCCCCCTTCTCTGTGGACACC 876
QY 301 TACCTCCACCTGCACCTGGCGACCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTCCTT 360
DB 877 TACCTCCACCTGCACCTGGCGACCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTCCTT 936
QY 361 TTTGCCTCCAAATCTGTCTCCATCTGACCCCTCTGCTCATCGGACCTGGGACGCTACCTC 420
DB 937 TTTGCCTCCAAATCTGTCTCCATCTGACCCCTCTGCTCATCGGACCTGGGACGCTACCTC 996
QY 421 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 480
DB 997 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 1056
QY 481 CTGGTGAGCACCTGGGTTGTGGGCTGGCCAGCTTTTGTCTCCCTCTGGCCCTATTATATC 540
DB 1057 CTGGTGAGCACCTGGGTTGTGGGCTGGCCAGCTTTTGTCTCCCTCTGGCCCTATTATATC 1116
QY 541 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGGCCGGCCCTTACACCACC 600
DB 1117 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGGCCGGCCCTTACACCACC 1176
QY 601 ATCCTCATGGGCATCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 660

Db 1177 ATCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 1236
QY 661 ATCCACCGCCAGGTCAAACGAGCAGCAGCAGGCACTGACCAATAACAAGTTGCGACAGGCA 720
Db 1237 ATCCACCGCCAGGTCAAACGAGCAGCAGCAGGCACTGACCAATAACAAGTTGCGACAGGCA 1296
QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCGTTTCCAGGAG 780
Db 1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCGTTTCCAGGAG 1356
QY 781 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGGATTTCATCTGAGCCAGTCAGT 840
Db 1357 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGGATTTCATCTGAGCCAGTCAGT 1416
QY 841 GCTGCCACCAACCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 900
Db 1417 GCTGCCACCAACCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 1476
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGGCCA 960
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGGCCA 1536
QY 961 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTATCGGAATTTGGGAAGGTGACTCGAATG 1020
Db 1537 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTATCGGAATTTGGGAAGGTGACTCGAATG 1596
QY 1021 TGTGTTGCTGTGTTCCCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1080
Db 1597 TGTGTTGCTGTGTTCCCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1656
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1140
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1716
QY 1141 CTCATATGTTGCATCAACCTCTGCTCTATGACGCCATGAACCGCCAAATTCGSCAAAGCA 1200
Db 1717 CTCATATGTTGCATCAACCTCTGCTCTATGACGCCATGAACCGCCAAATTCGSCAAAGCA 1776
QY 1201 TATGGCTCCATTTTAAAGAGAGGCCCCCGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1260
Db 1777 TATGGCTCCATTTTAAAGAGAGGCCCCCGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1836
QY 1261 CCTAGTCACCAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1306
Db 1837 CCTAGTCACCAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1882

RESULT 4

US-09-764-886-84/c
; Sequence 84, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT202
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-886-84

Query Match 99.6%; Score 1306; DB 10; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGAATGCTAGGTTCTGATTCCTCTTCTTCCACCCCTGCTCTTTAGCCTCTATC 60

Db 1470 TTGAATGCTAGGTTCTGATTCCTCTTCTTCCACCCCTCTTTCAGCCTCTATC 1411
QY 61 ATGTGGAACAGCTCTGACGCCAACTTCTCTGTACTACATGAGTCTGTCTGGGCTATCGT 120
Db 1410 ATGTGGAACAGCTCTGACGCCAACTTCTCTGTACTACATGAGTCTGTCTGGGCTATCGT 1351
QY 121 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 180
Db 1350 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 1291
QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCCAAAGCTCCGTACCCGATTCAACTGCTCATAGCC 240
Db 1290 ACCCTACTGGCCTTGGCCATCCAGCCCCAAAGCTCCGTACCCGATTCAACTGCTCATAGCC 1231
QY 241 AACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTTCAGGCCCTTCTCTGTGGACACC 300
Db 1230 AACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTTCAGGCCCTTCTCTGTGGACACC 1171
QY 301 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGTATTTGGGCTCCTCCTT 360
Db 1170 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGTATTTGGGCTCCTCCTT 1111
QY 361 TTTGCTCCAAATTTCTGTCTCCATCCTGACCCCTCTGCTCATCGCACTGGACGCTACCTC 420
Db 1110 TTTGCTCCAAATTTCTGTCTCCATCCTGACCCCTCTGCTCATCGCACTGGACGCTACCTC 1051
QY 421 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGGATAGTCTGGCA 480
Db 1050 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGGATAGTCTGGCA 991
QY 481 CTGGTGACCACTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTTGGCCTATTATATC 540
Db 990 CTGGTGACCACTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTTGGCCTATTATATC 931
QY 541 CTGGTACCTGTAGTCTGCACCTGACGCTTTGACCGCATCCGAGCCCGGCTTACACCAACC 600
Db 930 CTGGTACCTGTAGTCTGCACCTGACGCTTTGACCGCATCCGAGCCCGGCTTACACCAACC 871
QY 601 ATCTCATGGGCTACTCTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 660
Db 870 ATCTCATGGGCTACTCTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 811
QY 661 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATAACAAGTTGCGACAGGCA 720
Db 810 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATAACAAGTTGCGACAGGCA 751
QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 780
Db 750 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 691
QY 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTCACTGAGCCAGTCACT 840
Db 690 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTCACTGAGCCAGTCACT 631
QY 841 GCTGCCACCAACCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 900
Db 630 GCTGCCACCAACCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 571
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAAGCCAGGCCA 960
Db 570 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAAGCCAGGCCA 511
QY 961 ATTAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
Db 510 ATTAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG 451
QY 1021 TGTGTTGCTGTGTTCTCTGCTTTTGGCCTGAGTACATCCCTTCTTGTGCTCAACATT 1080
Db 450 TGTGTTGCTGTGTTCTCTGCTTTTGGCCTGAGTACATCCCTTCTTGTGCTCAACATT 391
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTCCAACTCACCTGG 1140
Db 390 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTCCAACTCACCTGG 331

481 CTGGTGAACAGCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 540
1057 CTGGTGAACAGCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 1116
541 CTGGTACCTGTAGTCTGCACCTGTGAGCTTTGACCGCATCCGAGCGCGCCTTACACCA 600
1117 CTGGTACCTGTAGTCTGCACCTGTGAGCTTTGACCGCATCCGAGCGCGCCTTACACCA 1176
601 ATCCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 660
1177 ATCCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 1236
661 ATCCACCGCCAGGTCAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 720
1237 ATCCACCGCCAGGTCAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 1296
721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 780
1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 1356
781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 840
1357 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 1416
841 GCTGCCACCAACCCAGACCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 900
1417 GCTGCCACCAACCCAGACCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 1476
901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGGATCTGCCAAAGCCAGCCA 960
1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGGATCTGCCAAAGCCAGCCA 1536
961 ATTAAGGAGCCAGAGAGCTCCGGATTTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
1537 ATTAAGGAGCCAGAGAGCTCCGGATTTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
1021 TGTTTTGCTGTCTCCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTCTGCTCAACATT 1080
1597 TGTTTTGCTGTCTCCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTCTGCTCAACATT 1656
1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACTGG 1140
1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACTGG 1716
1141 CTCAATGGTTGCATCAACCTGTGCTCTATGAGCCATGAAACCGCAATTCGCGCAAGCA 1200
1717 CTCAATGGTTGCATCAACCTGTGCTCTATGAGCCATGAAACCGCAATTCGCGCAAGCA 1776
1201 TATGGTCCATTTTAAAGAGAGGCGCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1260
1777 TATGGTCCATTTTAAAGAGAGGCGCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1836
1261 CCTAGTACCAAGATTTCAGGACTGTCTCCTCCAGGACCAAGTGGC 1306
1837 CCTAGTACCAAGATTTCAGGACTGTCTCCTCCAGGACCAAGTGGC 1882

RESULT 8

US-10-073-865-130
; Sequence 130, Application US/10073865
; Publication No. US2003004904A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ209C1
; CURRENT APPLICATION NUMBER: US/10/073,865
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 2046

TYPE: DNA
; ORGANISM: Homo sapiens
US-10-073-865-130
Query Match 99.6%; Score 1306; DB 15; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGAATGCTAGGTTCTGATTCCCTCTCTCTTCCACCTCTGCTTGTAGCCCTCTATC 60
Db 577 TTGAATGCTAGGTTCTGATTCCCTCTCTCTTCCACCTCTGCTTGTAGCCCTCTATC 636
QY 61 ATGTGGAACAGCTCTGACGCCAATCTTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT 120
Db 637 ATGTGGAACAGCTCTGACGCCAATCTTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT 696
QY 121 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCCGTGGGCAATGTGCTC 180
Db 697 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCCGTGGGCAATGTGCTC 756
QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
Db 757 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
QY 241 AACCTCAGACTGGCTGATCTCCTCTACTGACCGCTCCGTACCCGATTCAACCTGCTCATAGCC 300
Db 817 AACCTCAGACTGGCTGATCTCCTCTACTGACCGCTCCGTACCCGATTCAACCTGCTCATAGCC 876
QY 301 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTCTT 360
Db 877 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTCTT 936
QY 361 TTTGCCCTCCAAATTTCTGCTCCTGACCCCTCTGCTCATGCGACTGGGACGCTACTCTC 420
Db 937 TTTGCCCTCCAAATTTCTGCTCCTGACCCCTCTGCTCATGCGACTGGGACGCTACTCTC 996
QY 421 CTCAATGGCCACCCCTAAGCTTTTCCCAAAGTTTTCAGTGGCAAGGGGATAGTGTGGCA 480
Db 997 CTCAATGGCCACCCCTAAGCTTTTCCCAAAGTTTTCAGTGGCAAGGGGATAGTGTGGCA 1056
QY 481 CTGGTGAACAGCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 540
Db 1057 CTGGTGAACAGCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 1116
QY 541 CTGGTACCTGTAGTCTGCACCTGTGAGCTTTGACCGCATCCGAGCGCGCCTTACACCA 600
Db 1117 CTGGTACCTGTAGTCTGCACCTGTGAGCTTTGACCGCATCCGAGCGCGCCTTACACCA 1176
QY 601 ATCCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 660
Db 1177 ATCCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 1236
QY 661 ATCCACCGCCAGGTCAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 720
Db 1237 ATCCACCGCCAGGTCAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 1296
QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 780
Db 1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 1356
QY 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 840
Db 1357 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 1416
QY 841 GCTGCCACCAACCCAGACCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 900
Db 1417 GCTGCCACCAACCCAGACCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 1476
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGGATCTGCCAAAGCCAGGCA 960
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGGATCTGCCAAAGCCAGGCA 1536
QY 961 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020

Db 1537 ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTGGGAAGGTGACTCGAATG 1596
QY 1021 TGTTTGTGCTGTTCCTCTGCTTGGCCCTGAGCTACATCCCTTCTTTGCTGTCTCAACATT 1080
Db 1597 TGTTTGTGCTGTTCCTCTGCTTGGCCCTGAGCTACATCCCTTCTTTGCTGTCTCAACATT 1656
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCTCAACCTCACCTGG 1140
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCTCAACCTCACCTGG 1716
QY 1141 CTCAATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAAATTCGCGCAAGCA 1200
Db 1717 CTCAATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAAATTCGCGCAAGCA 1776
QY 1201 TATGGCTCCATTATAAAGAGGCCCCGGAGTTTCCATFAGGCTCCATTAGAACTGTGAC 1260
Db 1777 TATGGCTCCATTATAAAGAGGCCCCGGAGTTTCCATFAGGCTCCATTAGAACTGTGAC 1836
QY 1261 CCTAGTCACCAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1306
Db 1837 CCTAGTCACCAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1882

RESULT 9

US-10-103-313-592
; Sequence 592, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ07C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 592
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-313-592

Query Match 99.6%; Score 1306; DB 15; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATGCTAGGTTCTGATTCCTCTTCTCCTCTTCCACCCCTTCTTTAGCCCTATC 60
Db 577 TTGAATGCTAGGTTCTGATTCCTCTTCTCCTTCCACCCCTTCTTTAGCCCTATC 636
QY 61 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTCTACCATGATGCTGTGCTGGCTATCGT 120
Db 637 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTCTACCATGATGCTGTGCTGGCTATCGT 696
QY 121 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACAGGACCCGTGGCAATGTGCTC 180
Db 697 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACAGGACCCGTGGCAATGTGCTC 756
QY 181 ACCCTACTGSCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
Db 757 ACCCTACTGSCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
QY 241 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTCAGCCCTTCTCTGTGGACACC 300
Db 817 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTCAGCCCTTCTCTGTGGACACC 876
QY 301 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGTCAGGGTATTTGGGCTCCTCCTT 360
Db 877 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGTCAGGGTATTTGGGCTCCTCCTT 936
QY 361 TTTGGCTCAATTTCTGTCTCCATCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 420

Db 937 TTTGCCCTCCAATTCTGTCTCCAATCCTGACCCCTCTGCCCTCATCGCACTGGACGCTACCTC 996
QY 421 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATAGTCTGGCA 480
Db 997 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATAGTCTGGCA 1056
QY 481 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGTCTCCCTCTCTGGCCTATTATATC 540
Db 1057 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGTCTCCCTCTCTGGCCTATTATATC 1116
QY 541 CTGGTACCTGTAGTCTGCACCTGTGAGCTTTGACCGCATCCGAGGCGGCTTACACCAACC 600
Db 1117 CTGGTACCTGTAGTCTGCACCTGTGAGCTTTGACCGCATCCGAGGCGGCTTACACCAACC 1176
QY 601 ATCCTCATGGSCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTCCT 660
Db 1177 ATCCTCATGGSCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTCCT 1236
QY 661 ATCCACCGCCAGGTCAAACGAGCAGCAGCAGGCACTGGACCAATAACAAGTTGCGACAGGCA 720
Db 1237 ATCCACCGCCAGGTCAAACGAGCAGCAGCAGGCACTGGACCAATAACAAGTTGCGACAGGCA 1296
QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCCTGGTCGTTTCCAGGAG 780
Db 1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCCTGGTCGTTTCCAGGAG 1356
QY 781 CTGGACAGCAGCTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCACT 840
Db 1357 CTGGACAGCAGCTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCACT 1416
QY 841 GCTGCCACACCCAGACCCCTGGAAAGGGGACTCATCAGAAAGTGGGAGACCAAGTCAACAGC 900
Db 1417 GCTGCCACACCCAGACCCCTGGAAAGGGGACTCATCAGAAAGTGGGAGACCAAGTCAACAGC 1476
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCCA 960
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCCA 1536
QY 961 ATTAAGGAGCCAGAAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
Db 1537 ATTAAGGAGCCAGAAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
QY 1021 TGTTTGTGCTGCTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1080
Db 1597 TGTTTGTGCTGCTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1656
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCGCAACCTCACCTGG 1140
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCGCAACCTCACCTGG 1716
QY 1141 CTCAATGGTTGCATCAACCCCTGTCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1200
Db 1717 CTCAATGGTTGCATCAACCCCTGTCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1776
QY 1201 TATGGCTCCATTATAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1260
Db 1777 TATGGCTCCATTATAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGAC 1836
QY 1261 CCTAGTCACCAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1306
Db 1837 CCTAGTCACCAGAAATTCAGGACTGTCTCCTCCAGGACCAAAAGTGGC 1882

RESULT 10

US-09-826-508-37
; Sequence 37, Application US/09826508
; Patent No. US20010025099A1
; GENERAL INFORMATION:
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Lisa Vawter
; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
; TITLE OF INVENTION: and Polynucleotides
; FILE REFERENCE: GP-70744USB

QY	49	TTAGCCTCTATCATGTGGAACAGACTCTGACGCCAACATTCTCTCGTACCATGAGTCTGTG	108
Db	64	TCAGCCTCTATCATGTGGAACAGACTCTGACGCCAACATTCTCTCGTACCATGAGTCTGTG	123
QY	109	CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGCACCGTG	168
Db	124	CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGCACCGTG	183
QY	169	GGCAATGTGCTCACCCCTACTGGCCCTTGGCCATCCAGGCCCAAGCTCCGTACCCGATTCAAC	228
Db	184	GGCAATGTGCTCACCCCTACTGGCCCTTGGCCATCCAGGCCCAAGCTCCGTACCCGATTCAAC	243
QY	229	CTGCTCATAGCCAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC	288
Db	244	CTGCTCATAGCCAACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC	303
QY	289	TCTGTGGACACCTACCTCCACCTGCACCTGGCGCACCCGGTGCACCTTCTGTCAGGGTATTT	348
Db	304	TCTGTGGACACCTACCTCCACCTGCACCTGGCGCACCCGGTGCACCTTCTGTCAGGGTATTT	363
QY	349	GGGCTCCTCCTTTTGGCTCCAAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTG	408
Db	364	GGGCTCCTCCTTTTGGCTCCAAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTG	423
QY	409	GGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCCCAAGTTTTCAGTGCCCAAGGGG	468
Db	424	GGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCCCAAGTTTTCAGTGCCCAAGGGG	483
QY	469	ATAGTGTGGCACTGGTGAGCACCTGGGTGTGGGGCTGGCCAGCTTTGCTCCCCCTCTGG	528
Db	484	ATAGTGTGGCACTGGTGAGCACCTGGGTGTGGGGCTGGCCAGCTTTGCTCCCCCTCTGG	543
QY	529	CCTATTTATATCCTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGGCCGG	588
Db	544	CCTATTTATATCCTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGGCCGG	603
QY	589	CCTTACACCACCATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATC	648
Db	604	CCTTACACCACCATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATC	663
QY	649	TTCTATTGCCTCATCCACGCCAGGTCAAACGAGCAGCAGCAGGCACTGGACCAATACAAG	708
Db	664	TTCTATTGCCTCATCCACGCCAGGTCAAACGAGCAGCAGCAGGCACTGGACCAATACAAG	723
QY	709	TTGCGACAGGCAAGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT	768
Db	724	TTGCGACAGGCAAGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT	783
QY	769	CGTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCT	828
Db	784	CGTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCT	843
QY	829	GAGCCAGTCAGTGTGCCACCA CCCAGACCCTGGAAAGGGGACTCATCAGAAAGTGGGAGAC	888
Db	844	GAGCCAGTCAGTGTGCCACCA CCCAGACCCTGGAAAGGGGACTCATCAGAAAGTGGGAGAC	903
QY	889	CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCC	948
Db	904	CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCC	963

Query Match	95.8%;	Score 1256.4;	DB 15;	Length 1546;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1257;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
QY	49	TTAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTG	108	
Db	79	TCAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTG	138	
QY	109	CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGTGGCTGTGACAGGCACCGTG	168	
Db	139	CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGTGGCTGTGACAGGCACCGTG	198	
QY	169	GGCAATGTGCTCACCCCTACTGGCCCTTGCCCATCCAGCCCCAAGCTCCGTACCCGATTCAAC	228	
Db	199	GGCAATGTGCTCACCCCTACTGGCCCTTGCCCATCCAGCCCCAAGCTCCGTACCCGATTCAAC	258	
QY	229	CTGCTCTATAGCCAAACCTCACACTGGCTGATCTCCTCTACTGCAAGCTCCTTCAGCCCTTC	288	
Db	259	CTGCTCTATAGCCAAACCTCACACTGGCTGATCTCCTCTACTGCAAGCTCCTTCAGCCCTTC	318	
QY	289	TCTGTGGACACCTACCTCCACCTGCCTGGCGCACCGGTGCCACCTTCTGCAGGGTATTT	348	
Db	319	TCTGTGGACACCTACCTCCACCTGCCTGGCGCACCGGTGCCACCTTCTGCAGGGTATTT	378	

QY	349	GGGCTCCTCCTTTTGGCTCCAAATTTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTG	408
Db	379	GGGCTCCTCCTTTTGGCTCCAAATTTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTG	438
QY	409	GGACGCTACCTCCTCATTTGGCCACCCCTAAGCTTTTCCCCAAAGTTTTCAGTGCCAAAGGG	468
Db	439	GGACGCTACCTCCTCATTTGGCCACCCCTAAGCTTTTCCCCAAAGTTTTCAGTGCCAAAGGG	498
QY	469	ATAGTGTGGCACTGGTGGAGCACCTGGGTTGTGGGCGTGGCCAGCTTTGTCTCCCTCTGG	528
Db	499	ATAGTGTGGCACTGGTGGAGCACCTGGGTTGTGGGCGTGGCCAGCTTTGTCTCCCTCTGG	558
QY	529	CCTATTATATCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	588
Db	559	CCTATTATATCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	618
QY	589	CCTTACACCACCATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGGCATC	648
Db	619	CCTTACACCACCATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGGCATC	678
QY	649	TTCTATTGCTCATCCACGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAG	708
Db	679	TTCTATTGCTCATCCACGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAG	738
QY	709	TTGGACAGGCAAGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT	768
Db	739	TTGGACAGGCAAGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT	798
QY	769	CGTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCT	828
Db	799	CGTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCT	858
QY	829	GAGCCAGTCAGTCTGCCACCAACCAGACCCCTGGAAGSGGACTCATCAGAAAGTGGGAGAC	888
Db	859	GAGCCAGTCAGTCTGCCACCAACCAGACCCCTGGAAGSGGACTCATCAGAAAGTGGGAGAC	918
QY	889	CAGATCAACAGCAAGAGACTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCC	948
Db	919	CAGATCAACAGCAAGAGACTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCC	978
QY	949	AAAGCCCAGCCAAATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAG	1008
Db	979	AAAGCCCAGCCAAATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAG	1038
QY	1009	GTGACTCGAATGTGTTTGTGCTGTGTTTCTCTGCTTTTGCCTGAGCTACATCCCCCTCTTG	1068
Db	1039	GTGACTCGAATGTGTTTGTGCTGTGTTTCTCTGCTTTTGCCTGAGCTACATCCCCCTCTTG	1098
QY	1069	CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCC	1128
Db	1099	CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCC	1158
QY	1129	AACCTCACCTGGCTCAATGTTGTCATCAACCCCTGTGCTCTATGCAGCCATGAACCCGCAA	1188
Db	1159	AACCTCACCTGGCTCAATGTTGTCATCAACCCCTGTGCTCTATGCAGCCATGAACCCGCAA	1218
QY	1189	TTCCGCCAAGCATATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT	1248
Db	1219	TTCCGCCAAGCATATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT	1278
QY	1249	TAGAACTGTGACCCCTAGTACCAAGAAATTCAGGACTGTGTCTCCTCCAGGACCAAGTGCC	1306
Db	1279	TAGAACTGTGACCCCTAGTACCAAGAAATTCAGGACTGTGTCTCCTCCAGGACCAAGTGCC	1336

```

; TITLE OF INVENTION: No. US20020187947A1el. Gene
; FILE REFERENCE: 4-31328A/H026
; CURRENT APPLICATION NUMBER: US/09/798,710
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/XXX,XXX
; PRIOR FILING DATE: 2000-03-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-09-798-710-1

```

Query Match 95.8%; Score 1256.4; DB 9; Length 1595;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1257; Conservative 0; Mismatches 1; Indels 0;

QY	49	TTAGCCTCTATCATGTGGAAACAGCTCTGACGCCAACTTCTCCTGTCTACCATGAGTCTGTG	108
DB	128	TCAGCCCTCTATCATGTGGAAACAGCTCTGACGCCAACTTCTCCTGTCTACCATGAGTCTGTG	187
QY	109	CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGTGGTGGCTGTGACAGGCACCCGTG	168
DB	188	CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGTGGTGGCTGTGACAGGCACCCGTG	247
QY	169	GGCAATGTGCTCACCCCTACTGGCCCTTGGCCATCCAGGCCAAAGCTCCGTACCCGATTCAAC	228
DB	248	GGCAATGTGCTCACCCCTACTGGCCCTTGGCCATCCAGGCCAAAGCTCCGTACCCGATTCAAC	307
QY	229	CTGCTCATAGCCAAACCTCACACTGGCTGATCTCCTCTACTGTCACGCTCCTTCAGCCCTTC	288
DB	308	CTGCTCATAGCCAAACCTCACACTGGCTGATCTCCTCTACTGTCACGCTCCTTCAGCCCTTC	367
QY	289	TCTGTGGACACCTACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGCAGGGTATTT	348
DB	368	TCTGTGGACACCTACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGCAGGGTATTT	427
QY	349	GGGCTCCTCCTTTTGGCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTG	408
DB	428	GGGCTCCTCCTTTTGGCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTG	487
QY	409	GGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTTTCCCAAGTTTTTCAGTGCCCAAGGGG	468
DB	488	GGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTTTCCCAAGTTTTTCAGTGCCCAAGGGG	547
QY	469	ATAGTGTGGCACTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCCCTCTGG	528
DB	548	ATAGTGTGGCACTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCCCTCTGG	607
QY	529	CCTATTTTATCCTGGTACCTGTAGTCTGCACCTTGACCTTTGACCGCATCCGAGGCCGG	588
DB	608	CCTATTTTATCCTGGTACCTGTAGTCTGCACCTTGACCTTTGACCGCATCCGAGGCCGG	667
QY	589	CCTTACACCAATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATC	648
DB	668	CCTTACACCAATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATC	727
QY	649	TTCTATTGCTCATTCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCAATACAAG	708
DB	728	TTCTATTGCTCATTCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCAATACAAG	787
QY	709	TTGCGACAGGCAAGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT	768
DB	788	TTGCGACAGGCAAGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT	847
QY	769	CGTTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCT	828
DB	848	CGTTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCT	907
QY	829	GAGCCAGTCAGTGTGCTGCCACCCACCCAGACCCCTGGAGGGGACTCATCAGAAAGTGGGAGAC	888
DB	908	GAGCCAGTCAGTGTGCTGCCACCCACCCAGACCCCTGGAGGGGACTCATCAGAAAGTGGGAGAC	967

QY 889 CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCC 948
Db 968 CAGATCAACAGCAAGAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCC 1027
QY 949 AAAGCCAGCAATTAAGGAGCCAGAGAGCTCCGGATTCTTCAATCGGAATTGGGAAG 1008
Db 1028 AAAGCCAGCAATTAAGGAGCCAGAGAGCTCCGGATTCTTCAATCGGAATTGGGAAG 1087
QY 1009 GTGACTCGAATGTGTTTGTGCTGTGTTTCTCTGCTTTTGGCCCTGAGTACATCCCTTCTTG 1068
Db 1088 GTGACTCGAATGTGTTTGTGCTGTGTTTCTCTGCTTTTGGCCCTGAGTACATCCCTTCTTG 1147
QY 1069 CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCC 1128
Db 1148 CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCC 1207
QY 1129 AACCTCACCTGCTCAATGGTTGCATCAACCCCTGTGCTCTATGAGCCCATGAACGCCAA 1188
Db 1208 AACCTCACCTGCTCAATGGTTGCATCAACCCCTGTGCTCTATGAGCCCATGAACGCCAA 1267
QY 1189 TTCCGCCAAGCATATGGCTCCATTTTAAAGAGGGCCCCCGAGTTTCCATAGGCTCCAT 1248
Db 1268 TTCCGCCAAGCATATGGCTCCATTTTAAAGAGGGCCCCCGAGTTTCCATAGGCTCCAT 1327
QY 1249 TAGAACTGTGACCTAGTACCAAGAAATTCAGGACTGTCTCTCCAGGACCAAGTGGC 1306
Db 1328 TAGAACTGTGACCTAGTACCAAGAAATTCAGGACTGTCTCTCCAGGACCAAGTGGC 1385

RESULT 13

US-10-073-885-11
; Sequence 11, Application US/10073885
; Publication No. US20030096346A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ203C1
; CURRENT APPLICATION NUMBER: US/10/073,885
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1554)
; OTHER INFORMATION: n equals a,t,g, or c

US-10-073-885-11

Query Match 95.8%; Score 1255.6; DB 15; Length 1579;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1255; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 49 TTAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCCTGTGTACCATGAGTCTGTG 108
Db 100 TCAGCYKCTATCATGTGGAACAGCTCTGACGCCAACTTCTCCTGTGTACCATGAGTCTGTG 159
QY 109 CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGTGACAGGCCCGTG 168
Db 160 CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGTGACAGGCCCGTG 219
QY 169 GGCAATGTGCTACCCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAAC 228
Db 220 GGCAATGTGCTACCCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAAC 279
QY 229 CTGCTCATAGCCACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC 288
Db 280 CTGCTCATAGCCACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTC 339

QY 289 TCTGTGGACACCTACCTCCACCTGCACTGGCGCACCCGGTGCACACCTTCTGCAGGGTATTT 348
Db 340 TCTGTGGACACCTACCTCCACCTGCACTGGCGCACCCGGTGCACACCTTCTGCAGGGTATTT 399
QY 349 GGGCTCCTCCTTTTGGCTCCAAATTCGTCTCTCCATCCTGACCCCTCTGCCTCATCGCACTG 408
Db 400 GGGCTCCTCCTTTTGGCTCCAAATTCGTCTCTCCATCCTGACCCCTCTGCCTCATCGCACTG 459
QY 409 GGACGCTACCTCCTCATTTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGG 468
Db 460 GGACGCTACCTCCTCATTTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGG 519
QY 469 ATAGTGTGGCACTGGTGAGCACCTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTGG 528
Db 520 ATAGTGTGGCACTGGTGAGCACCTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTGG 579
QY 529 CCTATTTATATCCTGGTACCTGTAGTGTGCACCTGCGAGCTTTGACCGCATCCGAGGCCGG 588
Db 580 CCTATTTATATCCTGGTACCTGTAGTGTGCACCTGCGAGCTTTGACCGCATCCGAGGCCGG 639
QY 589 CCTTACACCACTCCTCATGGGCTACTATTGTGCTTGGGCTCAGCAGTGTGTGGCATC 648
Db 640 CCTTACACCACTCCTCATGGGCTACTATTGTGCTTGGGCTCAGCAGTGTGTGGCATC 699
QY 649 TTCTATTGCTCATCCACCGCCAGGTCAAAACGAGCAGCAGCAGCAATACAAAG 708
Db 700 TTCTATTGCTCATCCACCGCCAGGTCAAAACGAGCAGCAGCAGCAATACAAAG 759
QY 709 TTGCGACAGGCAAGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT 768
Db 760 TTGCGACAGGCAAGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGT 819
QY 769 CGTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCT 828
Db 820 CGTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCT 879
QY 829 GAGCCAGTCACTGCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGAC 888
Db 880 GAGCCAGTCACTGCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGAC 939
QY 889 CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCC 948
Db 940 CAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCC 999
QY 949 AAAGCCAGCCAAATTAAGGAGCCAGAGAGCTCCGGATTCTTCAATCGGAATTGGGAAG 1008
Db 1000 AAAGCCAGCCAAATTAAGGAGCCAGAGAGCTCCGGATTCTTCAATCGGAATTGGGAAG 1059
QY 1009 GTGACTCGAATGTGTTTGTGCTGTGTTTCTCTGCTTTTGGCCCTGAGTACATCCCTTCTTG 1068
Db 1060 GTGACTCGAATGTGTTTGTGCTGTGTTTCTCTGCTTTTGGCCCTGAGTACATCCCTTCTTG 1119
QY 1069 CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCC 1128
Db 1120 CTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCC 1179
QY 1129 AACCTCACCTGCTCAATGGTTGCATCAACCCCTGTGCTCTATGAGCCCATGAACGCCAA 1188
Db 1180 AACCTCACCTGCTCAATGGTTGCATCAACCCCTGTGCTCTATGAGCCCATGAACGCCAA 1239
QY 1189 TTCCGCCAAGCATATGGCTCCATTTTAAAGAGGGCCCCCGAGTTTCCATAGGCTCCAT 1248
Db 1240 TTCCGCCAAGCATATGGCTCCATTTTAAAGAGGGCCCCCGAGTTTCCATAGGCTCCAT 1299
QY 1249 TAGAACTGTGACCTAGTACCAAGAAATTCAGGACTGTCTCCTCCAGGACCAAGTGGC 1306
Db 1300 TAGAACTGTGACCTAGTACCAAGAAATTCAGGACTGTCTCCTCCAGGACCAAGTGGC 1357

RESULT 14

US-10-343-650A-45
; Sequence 45, Application US/10343650A
; Publication No. US20040067499A1

; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-1186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1191)
US-10-343-650A-45

Query Match 90.8%; Score 1191; DB 13; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGTATCGT 120
Dd 1 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGTATCGT 60

QY 121 TATGTTGAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 180
Dd 61 TATGTTGAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 120

QY 181 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGCTCATAGCC 240
Dd 121 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCACCTGCTCATAGCC 180

QY 241 AACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGGCTTCTCTGTGGACACC 300
Dd 181 AACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGGCTTCTCTGTGGACACC 240

QY 301 TACCTCCACCTGCACTGGCGCACCGGTGGCCACCTTCTGACGGPATTTGGGCTCCTCTT 360
Dd 241 TACCTCCACCTGCACTGGCGCACCGGTGGCCACCTTCTGACGGPATTTGGGCTCCTCTT 300

QY 361 TTTGGCTCCAATCTGTCTCCATCTGACCCCTCTGCTCATCGCACTGGACGCTACCTC 420
Dd 301 TTTGGCTCCAATCTGTCTCCATCTGACCCCTCTGCTCATCGCACTGGACGCTACCTC 360

QY 421 CTCATTGCCACCCCTAAGCTTTTTCGCCAAGTTTTCAGTGCCAGGGGATAGTCTGGCA 480
Dd 361 CTCATTGCCACCCCTAAGCTTTTTCGCCAAGTTTTCAGTGCCAGGGGATAGTCTGGCA 420

QY 481 CTGGTGAGCACCTGGTGTGGGGGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 540
Dd 421 CTGGTGAGCACCTGGTGTGGGGGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 480

QY 541 CTGGTACCTGTAGTCTGCACCTGCACTTTGACCGCATCCGAGCCGGCCTTACACACC 600
Dd 481 CTGGTACCTGTAGTCTGCACCTGCACTTTGACCGCATCCGAGCCGGCCTTACACACC 540

QY 601 ATCCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 660
Dd 541 ATCCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600

QY 661 ATCCACCGCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 720
Dd 601 ATCCACCGCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 660

QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTTCCAGGAG 780
Dd 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTTCCAGGAG 720

QY 781 CTGGACAGCAGGTTAGCATCAGGAGGAGCCAGTCCAGGATTTTCATCTGAGCCAGTCAGT 840
Dd 721 CTGGACAGCAGGTTAGCATCAGGAGGAGCCAGTCCAGGATTTTCATCTGAGCCAGTCAGT 780

QY 841 GCTGCCACCACTGAGCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 900
Dd 781 GCTGCCACCACTGAGCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 840

QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCA 960
Dd 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCA 900

QY 961 ATAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGTGAATG 1020
Dd 901 ATAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGTGAATG 960

QY 1021 TGTGTTGCTGTGTTCTCTGCTTTTGGCCCTGAGTACATCCCTTCTTGTGCTCAACATT 1080
Dd 961 TGTGTTGCTGTGTTCTCTGCTTTTGGCCCTGAGTACATCCCTTCTTGTGCTCAACATT 1020

QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1140
Dd 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1080

QY 1141 CTCAATGGTTGCATCAACCCCTGTGCTCTATGACGCCATGAACGCCCAATTCGCCAAGCA 1200
Dd 1081 CTCAATGGTTGCATCAACCCCTGTGCTCTATGACGCCATGAACGCCCAATTCGCCAAGCA 1140

QY 1201 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1251
Dd 1141 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191

RESULT 15
US-10-094-417-3
; Sequence 3, Application US/10094417
; Publication No. US20030045685A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik inc.
; TITLE OF INVENTION: No. US20030045685A1el Receptors
; FILE REFERENCE: 018781-008110US
; CURRENT APPLICATION NUMBER: US/10/094,417
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/802,803
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/276,649
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR35
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1188)
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR35
US-10-094-417-3

Query Match 90.6%; Score 1188; DB 15; Length 1188;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGTATCGT 120
Dd 1 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGTATCGT 60

QY	121	TATGTTGAGTTAGCTGGGGGTTGGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC	180		1141	TATGGCTCCATTTTAAAGAGGGCCCCCGGAGTTTCCATAGGCTCCAT	1188
Db	61	TATGTTGAGTTAGCTGGGGGTTGGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC	120				
QY	181	ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC	240				
Db	121	ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC	180				
QY	241	AACCTCACACTGGCTGATCTCCTCTACTGACGGTCTCTCTGTGGACACC	300				
Db	181	AACCTCACACTGGCTGATCTCCTCTACTGACGGTCTCTCTGTGGACACC	240				
QY	301	TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGACGGTATTTGGGCTCCTCCTT	360				
Db	241	TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGACGGTATTTGGGCTCCTCCTT	300				
QY	361	TTTGCCTCCAAATCTGTCTCCATCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC	420				
Db	301	TTTGCCTCCAAATCTGTCTCCATCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC	360				
QY	421	CTCATTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA	480				
Db	361	CTCATTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA	420				
QY	481	CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGTCTCCCTCTGGCCTATTTATATC	540				
Db	421	CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGTCTCCCTCTGGCCTATTTATATC	480				
QY	541	CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGCGCGCCTTACACCACC	600				
Db	481	CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGCGCGCCTTACACCACC	540				
QY	601	ATCCTCATGGGCATCTACTTTGTGCTTGGCTCAGCAGTGTGGCATCTTCTATTGCCTC	660				
Db	541	ATCCTCATGGGCATCTACTTTGTGCTTGGCTCAGCAGTGTGGCATCTTCTATTGCCTC	600				
QY	661	ATCCACCGCCAGGTCAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA	720				
Db	601	ATCCACCGCCAGGTCAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA	660				
QY	721	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCGTGCTTTCCAGGAG	780				
Db	661	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCGTGCTTTCCAGGAG	720				
QY	781	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTCTATCTGAGCCAGTCAGT	840				
Db	721	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTCTATCTGAGCCAGTCAGT	780				
QY	841	GCTGCCACCAACCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC	900				
Db	781	GCTGCCACCAACCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC	840				
QY	901	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGGCCA	960				
Db	841	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGGCCA	900				
QY	961	ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	1020				
Db	901	ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	960				
QY	1021	TGTTTGTGTTCTCTGCTTGGCCCTGAGCTACATCCCTTCTTGTCTGCTCAACATT	1080				
Db	961	TGTTTGTGTTCTCTGCTTGGCCCTGAGCTACATCCCTTCTTGTCTGCTCAACATT	1020				
QY	1081	CTGGATCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG	1140				
Db	1021	CTGGATCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG	1080				
QY	1141	CTCAATGGTTGCATCAACCTGTGCTCTATGAGCCCATGAACCGCCAATTCGCCAAGCA	1200				
Db	1081	CTCAATGGTTGCATCAACCTGTGCTCTATGAGCCCATGAACCGCCAATTCGCCAAGCA	1140				
QY	1201	TATGGCTCCATTTTAAAAAGAGGGCCCCCGGAGTTTCCATAGGCTCCAT	1248	QY			

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:14:09 ; Search time 3805.67 seconds
(without alignments)
10287.096 Million cell updates/sec

Title: US-10-029-436-1

Perfect score: 1311

Sequence: 1 ttgaatgctaggttctgtatt.....caggaccaaagtgccaggtta 1311

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1191	90.8	1191	29	AY404787 Homo sapi
2	1116.2	85.1	1187	29	AY404788 Pan trogl
3	889.2	67.8	1191	29	AY404789 Mus muscu
4	798.6	60.9	997	13	BX348812 BX348812

C	5	597	45.5	809	14	CD367121	CD367121	UI-H-FT2-
C	6	587	44.8	903	13	BX330186	BX330186	UI-H-FT2-
C	7	536	40.9	721	14	CD365430	CD365430	UI-H-FT2-
C	8	525	40.0	736	14	CD366881	CD366881	UI-H-FT2-
C	9	491	37.5	700	14	CD365279	CD365279	UI-H-FT2-
C	10	475	36.2	660	12	BM726245	BM726245	UI-E-EJ0-
C	11	464	35.4	1201	13	BX336527	BX336527	UI-E-EJ0-
C	12	448.4	34.2	496	13	BX097926	BX097926	UI-E-EJ0-
C	13	445.6	34.0	621	14	CD470995	CD470995	LeukoS5_3
C	14	442	33.7	650	14	CD366344	CD366344	UI-H-FT1-
C	15	426.6	32.5	660	10	BF667988	BF667988	602122233
C	16	419	32.0	542	12	BM254098	BM254098	515432 MA
C	17	415.4	31.7	829	10	BE958211	BE958211	601644675
C	18	412.8	31.5	553	12	BM258181	BM258181	522891 MA
C	19	409	31.2	588	12	BM680856	BM680856	UI-E-EJ0-
C	20	399.8	30.5	726	14	CF739045	CF739045	UI-M-HD0-
C	21	392.6	29.9	532	14	CD536450	CD536450	LeukoN6_7
C	22	392	29.9	499	12	BI773943	BI773943	465705 MA
C	23	391.4	29.9	498	14	CB221964	CB221964	11L22B6 B
C	24	386	29.4	474	12	BM105642	BM105642	509140 MA
C	25	368.8	28.1	533	10	BE502961	BE502961	hz81g02.x
C	26	367	28.0	526	12	BG232061	BG232061	naf32b01.
C	27	361.6	27.6	807	10	BF167811	BF167811	601774636
C	28	360	27.5	635	14	CD470023	CD470023	LeukoS4_1
C	29	354	27.0	518	9	AI392922	AI392922	tg10g11.x
C	30	353.2	26.9	458	14	CD464412	CD464412	LeukoN4_3
C	31	352	26.8	475	10	BF654980	BF654980	279349 MA
C	32	342.4	26.1	572	13	BX511990	BX511990	511990
C	33	342.2	26.1	588	14	CD465714	CD465714	LeukoN1_7
C	34	340.4	26.0	585	14	CD464304	CD464304	LeukoN4_3
C	35	339.2	25.9	588	14	CD470028	CD470028	LeukoS4_1
C	36	338.8	25.8	572	14	CD470901	CD470901	LeukoS5_3
C	37	337.2	25.7	584	14	CD536362	CD536362	LeukoN6_7
C	38	332.2	25.3	587	14	CD464888	CD464888	LeukoN4_5
C	39	323.6	24.7	551	14	CD464476	CD464476	LeukoN4_4
C	40	311.4	23.8	528	12	BG235994	BG235994	naf20f04.
C	41	299.2	22.8	368	10	BF706009	BF706009	280136 MA
C	42	288.2	22.0	497	10	AW213499	AW213499	um56b11.y
C	43	277	21.1	441	10	BE467421	BE467421	hz65f10.x
C	44	276	21.1	444	10	BF111095	BF111095	7n43d11.x
C	45	275.4	21.0	441	10	BE550808	BE550808	7b59c04.x

ALIGNMENTS

RESULT 1
AY404787
LOCUS
DEFINITION
1191 bp DNA linear GSS 16-DEC-2003
Homo sapiens GPR84 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY404787
VERSION
AY404787.1
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1191)
AUTHORS
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1191)
AUTHORS
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
source 1. .1191
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1. .>1191
/gene="GPR84"
/locus_tag="HCM2007"
ORIGIN
Query Match 90.8%; Score 1191; DB 29; Length 1191;
Best Local Similarity 100.0%; Pred. No. 7e-291;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGCTATCGT 120
Db 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGCTATCGT 60
QY 121 TATGTTGAGTTAGCTGGGGGTGTGTGGCTGTGACAGGACCGTGGGCAATGTC 180
Db 61 TATGTTGAGTTAGCTGGGGGTGTGTGGCTGTGACAGGACCGTGGGCAATGTC 120
QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
Db 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
QY 241 AACCTCACACTGCTGATCTCCTCTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 300
Db 181 AACCTCACACTGCTGATCTCCTCTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 240
QY 301 TACCTCCACCTGCACTGGCGCACCGGTGCGCACCTTCTGCAAGGATTTGGGCTCCTCCTT 360
Db 241 TACCTCCACCTGCACTGGCGCACCGGTGCGCACCTTCTGCAAGGATTTGGGCTCCTCCTT 300
QY 361 TTTGCCTCCAACTTCTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 420
Db 301 TTTGCCTCCAACTTCTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 360
QY 421 CTCATTGCCCACTTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATAGTGTGGCA 480
Db 361 CTCATTGCCCACTTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATAGTGTGGCA 420
QY 481 CTGGTGAGCACTGGGTTGTGGCGGTGCGCAGCTTTTGTCTCCCTCTGGCCTATTTATATC 540
Db 421 CTGGTGAGCACTGGGTTGTGGCGGTGCGCAGCTTTTGTCTCCCTCTGGCCTATTTATATC 480
QY 541 CTGGTACCTGTAGCTGCACCTGACCGCTTGACCGCATCCGAGCGCGCTTACACCAACC 600
Db 481 CTGGTACCTGTAGCTGCACCTGACCGCTTGACCGCATCCGAGCGCGCTTACACCAACC 540
QY 601 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCTC 660
Db 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCTC 600
QY 661 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 720
Db 601 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 660
QY 721 AGCATCCACTCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGCTTCCAGGAG 780
Db 661 AGCATCCACTCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGCTTCCAGGAG 720
QY 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT 840
Db 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAGT 780
QY 841 GCTGCCACCAACCAACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 900
Db 781 GCTGCCACCAACCAACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 840

QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 960
Db 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
QY 961 ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
Db 901 ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
QY 1021 TGTGTTGCTGTCTCTCTGCTTTGCGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1080
Db 961 TGTGTTGCTGTCTCTCTGCTTTGCGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
QY 1081 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1140
Db 1021 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1080
QY 1141 CTCAATGTTGCATCAACCTGTGCTCTATGCAGCCATGAACGCCAATTCGCCAAGCA 1200
Db 1081 CTCAATGTTGCATCAACCTGTGCTCTATGCAGCCATGAACGCCAATTCGCCAAGCA 1140
QY 1201 TATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 1251
Db 1141 TATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 1191
RESULT 2
AY404788 1187 bp DNA linear GSS 16-DEC-2003
LOCUS Pan troglodytes GPR84 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY404788
VERSION AY404788.1 GI:39760765
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 1187)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1187)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
source 1. .1187
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene <1. .>1187
/gene="GPR84"
/locus_tag="HCM2007"
ORIGIN
Query Match 85.1%; Score 1116.2; DB 29; Length 1187;
Best Local Similarity 94.4%; Pred. No. 6.7e-272;
Matches 1121; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 61 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGCTATCGT 120

Db 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
QY 121 TATGTTGCAGTTAGCTGGGGGTGGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC 180
Db 61 TATGTTGCAGTTAGCTGGGGGTGGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC 120
QY 181 ACCCTACTGSCCTTGGCCATCCAGCCAAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
Db 121 ACCCTACTGSCCTTGGCCATCCAGCCAAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
QY 241 AACCTCAGACTGGCTGATCTCCTCTACTGACAGCTCCTTCAGSCCTTCTCTGTGGACAC 300
Db 181 AACCTCAGACTGGCTGATCTCCTCTACTGACAGCTCCTTCAGSCCTTCTCTGTGGACAC 240
QY 301 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 360
Db 241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 300
QY 361 TTTGGCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGACGCTACCTC 420
Db 301 TTTGGCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGACGCTACCTC 360
QY 421 CTCATTGCCACCCCTAAGCTTTTTTCCCAAGTTTTTCAGTGCCAAAGGGGATAGTCTGGCA 480
Db 361 CTCATTGCCACCCCTAAGCTTTTTTCCCAAGTTTTTCAGTGCCAAAGGGGATAGTCTGGCA 420
QY 481 CTGGTGAGCACTGGGTTGTGGCGTGCGCCAGCTTTGCTCCCTCTGGCCTATTATATC 540
Db 421 CTGGTGAGCACTGGGTTGTGGCGTGCGCCAGCTTTGCTCCCTCTGGCCTATTATATC 480
QY 541 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCGGCCTTACACCAAC 600
Db 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCGGCCTTACACCAAC 540
QY 601 ATCCTCATGGGCATCTACTTTGTGCTTGGCCTGAGGCTGAGTGGCATCTTCTATTGGCTC 660
Db 541 ATCCTCATGGGCATCTACTTTGTGCTTGGCCTGAGGCTGAGTGGCATCTTCTATTGGCTC 600
QY 661 ATCCACCGCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 720
Db 601 ATCCACCGCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 660
QY 721 AGCATCCACTCCAACCATGTGGCCGAGCTGATGANGCNAATGCTGGTCTGTTTCCAGGAG 780
Db 661 AGCATCCACTCCAACCATGTGGCCGAGCTGATGANGCNAATGCTGGTCTGTTTCCAGGAG 720
QY 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAAT 840
Db 721 NTGGACAGCAGGTTAGCATCAGGAGGACCCNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780
QY 841 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGAGACCAGATCAACAGC 900
Db 781 NNNNNNACCAACCCAGACCNNTGGAAGGNNNNNTCAGAAAGTGGAGACCAGATCAACAGC 840
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCCA 960
Db 841 AAGAGAGNNAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCNCNTGCCAAAGCCAGCCCA 900
QY 961 ATTAAGGAGCCAGAAAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1020
Db 901 ATTAAGGAGCCAAAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
QY 1021 TGTTTTGCTGTGTTCTCTGCTTTTGGCCTGAGCTACATCCCTCTTGTGCTGCTCAACATT 1080
Db 961 TGTTTTGCTGTGTTCTCTGCTTTTGGCCTGAGCTACATCCCTCTTGTGCTGCTCAACATT 1020
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGTCACACCTCACCTGG 1140
Db 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGTCACACCTCACCTGG 1080
QY 1141 CTCATGTTGTCATCAACCCCTGTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1200
Db 1081 CTCAACGGTGTGATCAACCCCTGTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1140

QY 1201 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCA 1247
Db 1141 TATGGCTCCGTTTAAAAAGAGGGCCCCGGAGTTTCCGTAGGCTCCA 1187
RESULT 3
AY404789
LOCUS
DEFINITION
AY404789
genomic survey sequence.
VERSION
AY404789.1 GI:39760766
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1191)
AUTHORS
Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1191)
AUTHORS
Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..1191
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
gene
<1..>1191
/gene="GPR84"
/locus_tag="HCM2007"

ORIGIN

Query Match 67.8%; Score 889.2; DB 29; Length 1191;
Best Local Similarity 84.2%; Pred. No. 2.8e-214;
Matches 1002; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 61 ATGTGGAACAGCTGTGACGCCAACTTCTCCTGTACCATGAGTCTGTGCTGGGCTATCGT 120
Db 1 ATGTGGAACAGCTCAGATGCCAACTTCTCCTGTACCATGAGTCTGTGCTGGGCTATCGA 60
QY 121 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 180
Db 61 TACTTTGCAGTTATCTGGGGGTGGCAGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC 120
QY 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 240
Db 121 ACTCTGTGGCCTGGCCATTCTGTCCTCCTGCTGACAGGCACCGTTCACCTGCTCATTGCC 180
QY 241 AACCTCACACTGSGTGATCTCCTCTACTGCAGCTCCTTCAGCCCTTCTCTGTGGACACC 300
Db 181 AACCTCACCTGSGTGATCTACTCTACTGCAGCTCCTGCAGCCTTCTCTCGGTGGACACA 240
QY 301 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 360
Db 241 TACCTCCACCTCCATTGGCGTACCGGCGGCTTCTGTAGAAATTTTGGACTCCTCCTC 300
QY 361 TTTGGCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 420

Db 301 TTTACTTCCAAFTTGTCTCCATCTCACCCTCTGTCTCAATTGCTCTAGGACGCTACCTC 360
QY 421 CTCATTGCCACCTAAAGCTTTTCCCAAGTTTTCAGTGCCAGGGGATAGTGTGCA 480
Db 361 CTCATTGCCACCTAAAGCTTTTCCCAAGTTTTCAGTGCCAGGGGATCGTGTGCA 420
QY 481 CTGGTGAGCACCCTGGGTTGTGGCGTGCGCAGCTTTGCTCCCTCTGGCCTATTATATC 540
Db 421 CTGGTGGCAGCTGGGTTGTGGGGTGACAGCTTTGCCCCCTCTGGAATGTTTTTGC 480
QY 541 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGCCTTACACACC 600
Db 481 TTGGTGCCAGTTGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGCCTTACACACC 540
QY 601 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCCTC 660
Db 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGCGTGGCGTCTTCTACTGCCCTC 600
QY 661 ATCCACCGCCAGGTCAAACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 720
Db 601 ATCCACCGCCAGGTCAAACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 660
QY 721 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGTGCTGTTCCAGGAG 780
Db 661 AGCATCCGCTCTCATCAGGTGGTGGGACACAAGAACCATGCTGTGCTGCTTCCAGGAG 720
QY 781 CTGGACAGCAGGTAGCATCAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 840
Db 721 CTAGACAGCGGGGTTGCCTCAAGAGGCGCCAGCGAGGGGATTTCATCTGAGCCAGTCAGT 780
QY 841 GCTGCCACCAACCCAGACCTGGAAGGGGACTCATCAGAAGTGGGAGACACAGATCAACAGC 900
Db 781 GCTCGGACCAACCCAGACCTGGAAGGTGATTCTGTCAGAAGTGGGGGCCAGGGCATTAGA 840
QY 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGGCA 960
Db 841 AAGGAGCTCAACAGATCGCAGAGAGCCTTCCAGAAGTGCATCGCAAGCCCGGAA 900
QY 961 ATTAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTGGGAAGGTGACTCGAATG 1020
Db 901 ACTGCAGGAGCTCGCAGAGCCACAGATGCCCATCAGAGTTCGGAAGGTGACCCGATG 960
QY 1021 TGTTTTGCTGTCTCTGTCTTGGCCTGAGCTACATCCCTCTTCTGTCTCAACATT 1080
Db 961 TGCTTCGAGTGTCTCTGTCTTGGCCTCAGCTACATCCCTCTCTGTCTCAACATT 1020
QY 1081 CTGGATGCCAGAGTCCAGGCTCCCGGCTGGTCCACATGCTTGTGCTCCAACTCAGCTGG 1140
Db 1021 CTGGACGCCAGGGCGGTGCTCCACGAGTAGTGACATGCTGCTGCCAACTCAGCTGG 1080
QY 1141 CTCAATGTTGTCATCAACCTGTGCTCTATGAGCCATGACCGCAATTCGCGCCAGCA 1200
Db 1081 CTCAACAGCTGCATCAACCTGTGCTCTATGAGCCATGACCGCAATTCGCGCCAGCG 1140
QY 1201 TATGGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGTCCTATTA 1250
Db 1141 TATGGCTCCATCTGAAACGCGGGCCACAGAGTTTCCGCGGTTCCATTA 1190

RESULT 4
BX348812
LOCUS BX348812 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1029YE18 5-PRIME, mRNA sequence.
ACCESSION BX348812
VERSION BX348812.1 GI:30379347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 997)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6847.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAG028ZC10_CS02667_1&cluster=6847.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAG028ZC10_CS02667_1.
Location/Qualifiers
1. .997
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1029YE18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

ORIGIN

Query Match 60.9%; Score 798.6; DB 13; Length 997;
Best Local Similarity 98.7%; Pred. No. 2.5e-191;
Matches 823; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

QY 252 GGCTGATCTCTCTACTGCACGCTCCTTCCAGCCCTTCTCTGTGGACACCTACCTCCACCT 311
Db 15 GGCTGATCTCTCTACTGCACGCTCCTTCCAGCCCTTCTCTGTGGACACCTACCTCCACCT 74
QY 312 GCACCTGGGACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCTCTTGTGCCTCAA 371
Db 75 GCACCTGGGACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCTCTTGTGCCTCAA 134
QY 372 TTCTGTCTCCATCTGACCCCTCTGCTCATCGCACTGGGAGCTACCTCCTCATTTGCCCA 431
Db 135 TTCTGTCTCCATCTGACCCCTCTGCTCATCGCACTGGGAGCTACCTCCTCATTTGCCCA 194
QY 432 CCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGGGACTGGTGGAC 491
Db 195 CCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGGGACTGGTGGAC 254
QY 492 CTGGGTTGTGGCGTGGCCAGCTTTGACCGCATCCGAGCGCGCTTACACCACTCCTCATGG 551
Db 255 CTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGCTCCCTTATATATCTGTACCTGT 314
QY 552 AGTCTGACCTGCAGCTTTGACCGCATCCGAGCGCGCTTACACCACTCCTCATGG 611
Db 315 AGTCTGACCTGCAGCTTTGACCGCATCCGAGCGCGCTTACACCACTCCTCATGG 374
QY 612 CATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTTGCTCATCCACCGCA 671
Db 375 CATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTTGCTCATCCACCGCA 434
QY 672 GGTCAAACGAGCAGCAGGCACTGGACCAATACAAGTTGGGACAGGCAAGCATCCACTC 731
Db 435 GGTCAAACGAGCAGCAGGCACTGGACCAATACAAGTTGGGACAGGCAAGCATCCACTC 494
QY 732 CAACCATGTGGCCAGGACTGATGAGCCCATGCCTGGTCTGTTCCAGGAGCTGGACAGCAG 791
Db 495 CAACCATGTGGCCAGGACTGATGAGCCCATGCCTGGTCTGTTCCAGGAGCTGGACAGCAG 554
QY 792 GTTAGCATCAGGAGGACCCAGTGAAGGGGATTTTCATCTGAGCCAGTCACTGCTGCCACAC 851
Db 555 GTTAGCATCAGGAGGACCCAGTGAAGGGGATTTTCATCTGAGCCAGTCACTGCTGCCACAC 614
QY 852 CCAGACCTTGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGCAAGAGAGCTAA 911

Db 615 CCAGACCTGGAAGNGACTCATCAGAAGTGGGAGACCAGATCAACAGCAAGAGAGCTAA 674
QY 912 GCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCCAATTAAAGGAGC 971
Db 675 GCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAG-CCAGCCCAATTAAAGGAGC 733
QY 972 CAGAAGAGCTCCGGATTCTTTCATCGGAATTGGGAAGGTGACTCGAATGTGTTTGTGT 1031
Db 734 CAGAAGAGCTNCGNATTCTTTCATCGGGATTGGGGAGGTGACTCGAATGTGTTTGTGN 793
QY 1032 GTTCCTCTGCTTTGCCCTGAGCTACATCCCC-TTCTTGCTGCTCAACATTCTGG 1084
Db 794 GTTCCTCTGCTTTGCCCTGAGCTACATCCCCTTTCTTGCTGCTTAACATTCTTG 847

RESULT 5
CD367121/c
LOCUS
DEFINITION
UI-H-FT2-bjp-1-20-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjp-1-20-0-UI 3', mRNA sequence.
CD367121 GI:31151211
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 809)
AUTHORS
TITLE
JOURNAL
COMMENT
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. .809
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjp-1-20-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP FT2 is a subtraced cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtraced according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 45.5%; Score 597; DB 14; Length 809;
Best Local Similarity 99.2%; Pred. No. 3.2e-140;
Matches 630; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

QY 672 GGTCAACGAGCAGCAGCGCACTGGACCAATACAAGTTGGCAGGCAAGCATCCACTC 731
Db 809 GGTCAACGAGCAGCAGCGCACTGGACC-ATACAAGTTGGCAGGCAAGCATCCACTC 751

QY 732 CAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCGTTTCCAGGAGCTGGACAGCAG 791
Db 750 CANCCATGTGGCCAGGACTGATGAGNCCATGCCTGGTCGTTTCCAGGAGCTGGACAGCAG 691
QY 792 GTTAGCATCAGGAGACCCAGTGAGGGGATTTCATCTGAGCCAGTCAGTCTGCCACCAC 851
Db 690 GTTAGCATCAGGAGACCCAGTGAGGGGA-TTCATCTGAGCCAGTCAGTG-TGCCACCAC 633
QY 852 CCAGACCTCGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGCAAGAGAGCTAA 911
Db 632 CCAGACCTCGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGCAAGAGAGCTAA 573
QY 912 GCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCCAATTAAAGGAGC 971
Db 572 GCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCCAATTAAAGGAGC 513
QY 972 CAGAAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATGTGTTTGTGT 1031
Db 512 CAGAAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATGTGTTTGTGT 453
QY 1032 GTTCCTCTGCTTTGCCCTGAGCTACATCCCCTTTCTTGCTGCTCAACATTCTGGATGCCAG 1091
Db 452 GTTCCTCTGCTTTGCCCTGAGCTACATCCCCTTTCTTGCTGCTCAACATTCTGGATGCCAG 393
QY 1092 AGTCCAGGCTCCCCGGGTGGTCCACATGCTTGCTGCCAAACCTCACCTGGCTCAATGGTTG 1151
Db 392 AGTCCAGGCTCCCCGGGTGGTCCACATGCTTGCTGCCAAACCTCACCTGGCTCAATGGTTG 333
QY 1152 CATCAACCTCTGCTCTATGCGAGCCATGAACCGCCAAATTCGCCAAGCATATGGCTCCAT 1211
Db 332 CATCAACCTCTGCTCTATGCGAGCCATGAACCGCCAAATTCGCCAAGCATATGGCTCCAT 273
QY 1212 TTTAAAAAGAGGGCCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGACCCCTAGTCACCA 1271
Db 272 TTTAAAAAGAGGGCCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGACCCCTAGTCACCA 213
QY 1272 GAATTTCAGGACTGTCTCTCTCCAGGACCAAAAGTGGC 1306
Db 212 GAATTTCAGGACTGTCTCTCTCCAGGACCAAAAGTGGC 178

RESULT 6
BX330186/c
LOCUS
DEFINITION
BX330186 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI029YE18 3-PRIME, mRNA sequence.
BX330186
BX330186.1 GI:30307910
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 903)
AUTHORS
TITLE
JOURNAL
COMMENT
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6847.r For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAK055DE01NM1&cluster=6847.r>. Contact : Feng Liang Email : fliang@lifetech.com
URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0BAK055DE01NM1.
Location/Qualifiers
1. .903
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source
1. .903
/organism="Homo sapiens"
/mol_type="mRNA"

Db 242 TAGGTCATTAGAACTGTGACCCCTAGTACCAGAAATTCAGGACTGTCTCTCCAGGACC 183
QY 1299 AAAGTGGC 1306
Db 182 AAAGTGGC 175

RESULT 8
CD366881/c
LOCUS
DEFINITION
UI-H-FT2-bjp-k-21-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjp-k-21-0-UI 3', mRNA sequence.
CD366881
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 736)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjp-k-21-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtraced according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 40.0%; Score 525; DB 14; Length 736;
Best Local Similarity 99.3%; Pred. No. 5.8e-122;
Matches 558; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
QY 745 AGGACTGATCAGGCCATGCCCTGGTCGTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGA 804
Db 736 AGGACTGATCAGNCCATGCCCTGGTCGTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGA 677
QY 805 GGACCCAGTGGGGGATTTTCATCTGAGCCAGTCAGTGCTGCCACCACCCAGACCCCTGGAA 864
Db 676 GGACCCAGTGA-GGGATTTTCATCTGAGCCAGTCAGTGCTGCCACCACCCAGACCCCTGGAA 618
QY 865 GGGGACTCATCAGAAGTGGGAGACCATCATCAACAGCAAGAGAGCTAAGCAGATGGCAGAG 924
Db 617 -GGGACTCATCAGAAGT-GGAGACCAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAG 560

QY 925 AAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCAAATTAAGGAGCCAGAAGAGCTCCG 984
Db 559 AAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCAAATTAAGGAGCCAGAAGAGCTCCG 500
QY 985 GATTCTTCATCGGAATTTGGGAAGGTGACTCGAATGTGTTTTGCTGTGTTTCTCTGCTTT 1044
Db 499 GATTCTTCATCGGAATTTGGGAAGGTGACTCGAATGTGTTTTGCTGTGTTTCTCTGCTTT 440
QY 1045 GCCCTGAGCTACATCCCTTCTTCTGCTCTCAACATTTCTGGATGCAGAGTCCAGGCTCCC 1104
Db 439 GCCCTGAGCTACATCCCTTCTTCTGCTCTCAACATTTCTGGATGCAGAGTCCAGGCTCCC 380
QY 1105 CGGTTGTTCCACATGCTTGTCTGCCAACCTCACCTGGCTCAATGTTGTCATCAACCTGTG 1164
Db 379 CGGTTGTTCCACATGCTTGTCTGCCAACCTCACCTGGCTCAATGTTGTCATCAACCTGTG 320
QY 1165 CTCTATGACCCATGAACCGCCCAATTCGCCCAAGCATATGGCTCCATTTTAAAAGAGGG 1224
Db 319 CTCTATGACCCATGAACCGCCCAATTCGCCCAAGCATATGGCTCCATTTTAAAAGAGGG 260
QY 1225 CCCGGAGTTTCCATAGGCTCCATTAGAACTGTGACCCTAGTCACCAGAATTCAGGACTG 1284
Db 259 CCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGACCCTAGTCACCAGAATTCAGGACTG 200
QY 1285 TCTCTCTCAGGACCAAAAGTGGC 1306
Db 199 TCTCTCTCAGGACCAAAAGTGGC 178

RESULT 9
CD365279/c
LOCUS
DEFINITION
UI-H-FT2-bjj-k-21-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjj-k-21-0-UI 3', mRNA sequence.
CD365279
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 700)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Location/Qualifiers
1..700
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjj-k-21-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtraced according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa. TAG TISSUE=Human Lung Aveolar Macrophage TAG_LIB=UI-H-FT2 TAG_SEQ=GGCCATGCGG

ORIGIN

Query Match 37.5%; Score 491; DB 14; Length 700;
Best Local Similarity 99.1%; Pred. No. 2.4e-113;
Matches 524; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

QY 778 GAGCTGGACAGCAGGTTAGCATCAGGAGGAGCCAGTGGAGGATTCATCTGAGCCAGTC 837
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
700 GAGCTGGACAGCAGGTTAGCATCAGGAGGAGCCAGTGGAGGATTCATCTGAGCCAGTC 642

QY 838 AGTGTGTCACACACCCAGACCCCTGGAGGGGACTCATCAGAGTGGGAGCCAGATCAAC 897
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
641 AGT-CTGCCACACCCAGACCCCTGGAA-GGGACTCATCAGAGTGGGAGCCAGATCAAC 584

QY 898 AGCAAGAGAGTAAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAG 957
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
583 AGCAAGAGAGTAAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAG 524

QY 958 CCAATTAAGGAGCCAGAGAGCTCCGGATTCCTCATCGGAATTTGGGAAGGTGACTCGA 1017
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
523 CCAATTAAGGAGCCAGAGAGCTCCGGATTCCTCATCGGAATTTGGGAAGGTGACTCGA 464

QY 1018 ATGTGTTTCTGTTCTCTCTGTTTCCCTGAGTACATCCCTTCTTGTGCTCAAC 1077
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
463 ATGTGTTTCTGTTCTCTCTGTTTCCCTGAGTACATCCCTTCTTGTGCTCAAC 404

QY 1078 ATTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCAGATGTTGCTGCCAAGCTCACC 1137
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
403 ATTCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCAGATGTTGCTGCCAAGCTCACC 344

QY 1138 TGGCTCAATGTTGTCATCAACCTCTGCTCTATGCAGCCATGAACCGCCAAATTCGCCAA 1197
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
343 TGGCTCAATGTTGTCATCAACCTCTGCTCTATGCAGCCATGAACCGCCAAATTCGCCAA 284

QY 1198 GCATATGCTCCATTTTAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAAGACTGT 1257
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
283 GCATATGCTCCATTTTAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAAGACTGT 224

QY 1258 GACCTAGTACACAGAAATTCAGGACTGTCTCCTCCAGGACCAAGTGGC 1306
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
223 GACCTAGTACACAGAAATTCAGGACTGTCTCCTCCAGGACCAAGTGGC 175

RESULT 10
BM726245
LOCUS 660 bp mRNA linear EST 01-MAR-2002
DEFINITION UI-E-EJ0-aih-k-10-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone
UI-E-EJ0-aih-k-10-0-UI 5', mRNA sequence.

ACCESSION BM726245
VERSION BM726245.1 GI:19047578
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 660)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA
sequence: 599-657, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers
1..660
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-aih-k-10-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EJ0 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 36.2%; Score 475; DB 12; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.7e-109;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 832 CCAGTCAGTGTGCCACCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAG 891
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 CCAGTCAGTGTGCCACCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAG 60

QY 892 ATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAA 951
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 ATCAACAGCAAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAA 120

QY 952 GCCAGCCCAATTAAAGGAGCCAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTG 1011
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GCCAGCCCAATTAAAGGAGCCAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTG 180

QY 1012 ACTCGAATGTGTTTGTGTTCTCTCTGTTTCCCTGAGCTACATCCCTTCTGTCTG 1071
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 ACTCGAATGTGTTTGTGTTCTCTCTGTTTCCCTGAGCTACATCCCTTCTGTCTG 240

QY 1072 CTCACATCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAAC 1131
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTCACATCTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAAC 300

QY 1132 CTCACCTGGCTCAATGTTTGCATCAACCCCTGTGTCTATGCGAGCCATGAACCGCAATTC 1191
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 CTCACCTGGCTCAATGTTTGCATCAACCCCTGTGTCTATGCGAGCCATGAACCGCAATTC 360

QY 1192 CGCCAGCATATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 1251
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 CGCCAGCATATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 420

source	1. 496		Unpublished (2003)			
	/organism="Homo sapiens"		Other ESTs: LeukoS5_3_D04.b1_A027			
	/mol_type="mRNA"		Contact: Cordonnier-Pratt MM			
	/db_xref="taxon:9606"		Laboratory for Genomics and Bioinformatics			
	/clone="IMAGp998P215199 ; IMAGE:2108420"		The University of Georgia, Department of Plant Biology			
	/tissue type="B-cell, chronic lymphocytic leukemia"		Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA			
	/lab_host="DH10B"		Tel: 706 542 1860			
	/clone_lib="NCI CGAP CLL1"		Fax: 706 583 0210			
	/note="Vector: p773D-Pac (Pharmacia) with a modified		Email: mmpratt@uga.edu			
	polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA		Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in			
	was primed with a Not I - oligo(dT) primer [5'		the Human Genome Center, University of Tokyo Institute of Medical			
	TGTTACCAATCTGAAGTGGAGCGCGCATGCTTTTCTTTTCTTTTCTTTT		Science; tissue and RNA were prepared in the Department of Large			
	T 3']; double-stranded cDNA was ligated to Eco RI		Animal Medicine, University of Georgia; sequencing done in the			
	adaptors (Pharmacia), digested with Not I and cloned into		Laboratory for Genomics and Bioinformatics, University of Georgia.			
	the Not I and Eco RI sites of the modified p773 vector.		Sequence ends have been trimmed to exclude vector and regions below			
	Library is normalized, and was constructed by Bento		Phred quality 16. Three-prime sequences are presented as their			
	Soares and M.Fatima Bonaldo."		reverse complement and have been trimmed to exclude polyA.			
			Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).			
ORIGIN	Location/Qualifiers		FEATURES			
	1. 621		source			
	/organism="Equus caballus"		/organism="Equus caballus"			
	/mol_type="mRNA"		/mol_type="mRNA"			
	/strain="Dartmoor Pony"		/strain="Dartmoor Pony"			
	/db_xref="taxon:9796"		/db_xref="taxon:9796"			
	/clone="LeukoS5_3_D04_A027"		/clone="LeukoS5_3_D04_A027"			
	/sex="male"		/sex="male"			
	/tissue_type="blood"		/tissue_type="blood"			
	/cell_type="leukocytes"		/cell_type="leukocytes"			
	/lab_host="DH10B-T1 phage-resistant E. coli"		/lab_host="DH10B-T1 phage-resistant E. coli"			
	/clone_lib="Stimulated peripheral blood leukocytes S5"		/clone_lib="Stimulated peripheral blood leukocytes S5"			
	/note="Organ: circulatory system; Vector: pME18S-FL3;		/note="Organ: circulatory system; Vector: pME18S-FL3;			
	Site 1: XhoI; Site 2: XhoI; The library was prepared from		Site 1: XhoI; Site 2: XhoI; The library was prepared from			
	polyA+ RNA from equine peripheral blood leukocytes		polyA+ RNA from equine peripheral blood leukocytes			
	isolated from a healthy adult horse. The leukocytes were		isolated from a healthy adult horse. The leukocytes were			
	stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS.		stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS.			
	Double-stranded cDNA was cloned unidirectionally into		Double-stranded cDNA was cloned unidirectionally into			
	different DraIII sites of the pME18S-FL3 vector (5-prime		different DraIII sites of the pME18S-FL3 vector (5-prime			
	DraIII site is CACTGTGTG, 3-prime DraIII site is		DraIII site is CACTGTGTG, 3-prime DraIII site is			
	CACCATGTG). XhoI excises the cDNA insert."		CACCATGTG). XhoI excises the cDNA insert."			
ORIGIN						
	Query Match	34.0%;	Score 445.6;	DB 14;	Length 621;	
	Best Local Similarity	90.6%;	Pred. No. 7.4e-102;			
	Matches 475;	Conservative	0;	Mismatches 49;	Indels 0;	Gaps 0;
QY	44	CCTCTTTAGCCTCTATCATGTGGAACAGCTCTGACGCCAACATTTCTCTGCTGCTACCATGAGT	103			
Db	98	CCCCCTCAGCCTGCATCATGTGGAACAACTCTGTATGCCAACTTCTCTGCTGCTACCATGAGT	157			
QY	104	CTGTGCTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGGTGGTGGTGGCTGTGACAGGCA	163			
Db	158	CTGTGCTAGGCTATCGTTACGTTGCAGTTAGCTGGGGGGTGGTGGTGGCTGTGACAGGCA	217			
QY	164	CCGTGGGCAATGTGCTCACCTTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGAT	223			
Db	218	CCGTGGGCAACGTGCTCACCTTGTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCTGCT	277			
QY	224	TCAACCTGCTCATAGCCAACTCAGCTGGCTGATCTCTCTACTGCACGCTCTCTTCCAGC	283			
Db	278	TCAACCTGCTCATCGCCAACTCAGCTGGCCGATCTCTCTACTGCACGCTCTCTCCAGC	337			
QY	284	CCTTCTCTGTGGACACCTACTCCACCTGCACTGGCCGACCCGGTCCACCTCTCTGCAGGG	343			
Db	338	CCTTCTCGGTGGACACCTACTCCACCTGTACTGGCCGACCCGGCTACTCTCTGCAGAG	397			
QY	344	TATTGGGCTCCTCCTTTTGGCTCCAAATCTGTCTCTCCATCCTGACCTCTGCCTCATCG	403			
Db	398	TCCTTGGGCTCCTCCTCTTTGTCATCCAACTCTGTCTCTCCATCCTGACCTCTGCCTTAG	457			
QY	404	CACCTGGACGCTACCTCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCA	463			
Db	458	CCCTGGGACGTTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCA	517			

source	1. 496		Unpublished (2003)			
	/organism="Homo sapiens"		Other ESTs: LeukoS5_3_D04.g1_A027			
	/mol_type="mRNA"		Contact: Cordonnier-Pratt MM			
	/db_xref="taxon:9606"		Laboratory for Genomics and Bioinformatics			
	/clone="IMAGp998P215199 ; IMAGE:2108420"		The University of Georgia, Department of Plant Biology			
	/tissue type="B-cell, chronic lymphocytic leukemia"		Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA			
	/lab_host="DH10B"		Tel: 706 542 1860			
	/clone_lib="NCI CGAP CLL1"		Fax: 706 583 0210			
	/note="Vector: p773D-Pac (Pharmacia) with a modified		Email: mmpratt@uga.edu			
	polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA		Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in			
	was primed with a Not I - oligo(dT) primer [5'		the Human Genome Center, University of Tokyo Institute of Medical			
	TGTTACCAATCTGAAGTGGAGCGCGCATGCTTTTCTTTTCTTTTCTTTT		Science; tissue and RNA were prepared in the Department of Large			
	T 3']; double-stranded cDNA was ligated to Eco RI		Animal Medicine, University of Georgia; sequencing done in the			
	adaptors (Pharmacia), digested with Not I and cloned into		Laboratory for Genomics and Bioinformatics, University of Georgia.			
	the Not I and Eco RI sites of the modified p773 vector.		Sequence ends have been trimmed to exclude vector and regions below			
	Library is normalized, and was constructed by Bento		Phred quality 16. Three-prime sequences are presented as their			
	Soares and M.Fatima Bonaldo."		reverse complement and have been trimmed to exclude polyA.			
			Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).			
ORIGIN	Location/Qualifiers		FEATURES			
	1. 621		source			
	/organism="Equus caballus"		/organism="Equus caballus"			
	/mol_type="mRNA"		/mol_type="mRNA"			
	/strain="Dartmoor Pony"		/strain="Dartmoor Pony"			
	/db_xref="taxon:9796"		/db_xref="taxon:9796"			
	/clone="LeukoS5_3_D04_A027"		/clone="LeukoS5_3_D04_A027"			
	/sex="male"		/sex="male"			
	/tissue_type="blood"		/tissue_type="blood"			
	/cell_type="leukocytes"		/cell_type="leukocytes"			
	/lab_host="DH10B-T1 phage-resistant E. coli"		/lab_host="DH10B-T1 phage-resistant E. coli"			
	/clone_lib="Stimulated peripheral blood leukocytes S5"		/clone_lib="Stimulated peripheral blood leukocytes S5"			
	/note="Organ: circulatory system; Vector: pME18S-FL3;		/note="Organ: circulatory system; Vector: pME18S-FL3;			
	Site 1: XhoI; Site 2: XhoI; The library was prepared from		Site 1: XhoI; Site 2: XhoI; The library was prepared from			
	polyA+ RNA from equine peripheral blood leukocytes		polyA+ RNA from equine peripheral blood leukocytes			
	isolated from a healthy adult horse. The leukocytes were		isolated from a healthy adult horse. The leukocytes were			
	stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS.		stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS.			
	Double-stranded cDNA was cloned unidirectionally into		Double-stranded cDNA was cloned unidirectionally into			
	different DraIII sites of the pME18S-FL3 vector (5-prime		different DraIII sites of the pME18S-FL3 vector (5-prime			
	DraIII site is CACTGTGTG, 3-prime DraIII site is		DraIII site is CACTGTGTG, 3-prime DraIII site is			
	CACCATGTG). XhoI excises the cDNA insert."		CACCATGTG). XhoI excises the cDNA insert."			
ORIGIN						
	Query Match	34.2%;	Score 448.4;	DB 13;	Length 496;	
	Best Local Similarity	99.8%;	Pred. No. 1.3e-102;			
	Matches 449;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	49	TTAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG	108			
Db	47	TCAGCCTCTATCATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTG	106			
QY	109	CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGCTGGTGGTGGTGTGACAGGCCGCTG	168			
Db	107	CTGGGCTATCGTTATGTTGCAGTTAGCTGGGGGCTGGTGGTGGTGTGACAGGCCGCTG	166			
QY	169	GGCAATGTGCTACCCCTACTGGCCCTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAAC	228			
Db	167	GGCAATGTGCTACCCCTACTGGCCCTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAAC	226			
QY	229	CTGCTCATAGCCAACTCAGCTGGCTGATCTCTCTACTGACGCTCCTTCAGCCCTTC	288			
Db	227	CTGCTCATAGCCAACTCAGCTGGCTGATCTCTCTACTGACGCTCCTTCAGCCCTTC	286			
QY	289	TCTGTGGACACCTACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTT	348			
Db	287	TCTGTGGACACCTACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTT	346			
QY	349	GGGCTCCTCCTTTTGCCTCCCAATCTGTCTCCATCCCTGACCCCTCTGCCTCATCGCACTG	408			
Db	347	GGGCTCCTCCTTTTGCCTCCCAATCTGTCTCCATCCCTGACCCCTCTGCCTCATCGCACTG	406			
QY	409	GGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGG	468			
Db	407	GGACGCTACCTCCTCATTTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCACAGGGG	466			
QY	469	ATAGTGTGGCACTGGTGAGCACCTGGGTT	498			
Db	467	ATAGTGTGGCACTGGTGAGCACCTGGGTT	496			
RESULT 13						
LOCUS	CD470995		621 bp		linear	EST 04-JUN-2003
DEFINITION	LeukoS5_3_D04.g1_A027 Stimulated peripheral blood leukocytes S5					
	Equus caballus cDNA clone LeukoS5_3_D04_A027 5', mRNA sequence.					
ACCESSION	CD470995					
VERSION	CD470995.1					
KEYWORDS	EST.					
SOURCE	Equus caballus (horse)					
ORGANISM	Equus caballus					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.					
REFERENCE	1 (bases 1 to 621)					
AUTHORS	Vandenplas,M., Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S.,					
	Moore,J.N., Liang,C., Sun,F., Sullivan,R., Shah,M. and Pratt,L.H.					
TITLE	An EST database from equine (Equus caballus) stimulated peripheral					
	blood leukocytes					

QY 464 AGGGAFAGTGTGGCACTGGTACGACCTGGTGTGTGGCGTGGCCAGCTTTGTCTCCCC 523
|||||
Db 518 AGGGACAGTGTGGCACTGGTGGCACCTGGTGTGTGGGTGGCCAGCTTTGCCCTC 577
|||||
QY 524 TCTGGCCTATTATATCCTGGTACCTGTAGTCTGCACCTGCAGC 567
|||||
Db 578 TCTGGCCCATCTATATCTTGGTGCCGTAGTTTGCACCTGCAGC 621
|||||
RESULT 14
CD366344/c 650 bp mRNA linear EST 29-MAY-2003
LOCUS UI-H-FT1-bjt-i-04-0-UI.s1 NCI CGAP_F11 Homo sapiens cDNA clone
DEFINITION UI-H-FT1-bjt-i-04-0-UI 3', mRNA sequence.
ACCESSION CD366344
VERSION CD366344.1 GI:31150434
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 650)
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
source
1. .650
/location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjt-i-04-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_F11"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_F11 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 33.7%; Score 442; DB 14; Length 650;
Best Local Similarity 99.6%; Pred. No. 6.2e-101;
Matches 463; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 842 CTGCCACCACCCCTGGAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGCA 901
|||||

Db 638 CTGCCACCACCCAGACCCCTGGAA-GGGACTCATCAGAAGT-GGAGACCAGATCAACAGCA 581
QY 902 AGAGAGCTAACAGATGGCAGAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAAGCCAGCCAA 961
|||||
Db 580 AGAGAGCTAACAGATGGCAGAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAAGCCAGCCAA 521
|||||
QY 962 TTAAGGAGCCAGAGAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATGT 1021
|||||
Db 520 TTAAGGAGCCAGAGAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATGT 461
|||||
QY 1022 GTTTTGTGTCTCTCTCTCTCTTTTGGCCTGAGCTACATCCCTTCTTGTCTCAACATTC 1081
|||||
Db 460 GTTTTGTGTCTCTCTCTCTTTTGGCCTGAGCTACATCCCTTCTTGTCTCAACATTC 401
|||||
QY 1082 TGGATGCCAGAGTCCAGGCTCCCCGGTGGTCCACATGCTTGTGCCAACCTCACCTGGC 1141
|||||
Db 400 TGGATGCCAGAGTCCAGGCTCCCCGGTGGTCCACATGCTTGTGCCAACCTCACCTGGC 341
|||||
QY 1142 TCAATGGTTGCATCAACCCCTGTGTCTCTATGTCAGCCCATGAACCGCCAATTCCGCCAAGCAT 1201
|||||
Db 340 TCAATGGTTGCATCAACCCCTGTGTCTCTATGTCAGCCCATGAACCGCCAATTCCGCCAAGCAT 281
|||||
QY 1202 ATGGCTCCATTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGACC 1261
|||||
Db 280 ATGGCTCCATTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAGAACTGTGACC 221
|||||
QY 1262 CTAGTCACCAGAAATTCAGGACTGTCTCTCCAGGACCAAAAGTGGC 1306
|||||
Db 220 CTAGTCACCAGAAATTCAGGACTGTCTCTCCAGGACCAAAAGTGGC 176
|||||
RESULT 15
BF667988
LOCUS 602122233F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4279185 5',
DEFINITION mRNA sequence.
ACCESSION BF667988
VERSION BF667988.1 GI:11941883
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 660)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1104 row: a column: 10
High quality sequence stop: 597.
FEATURES
source
1. .660
/location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4279185"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_56"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgacctggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3', and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-DT(30)BN-3',

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:04:24 ; Search time 4851.11 Seconds
(without alignments)
10641.181 Million cell updates/sec

Title: US-10-029-436-1_COPY_61_1251
Perfect score: 1191
Sequence: 1 atgtggaacagctctgacgc.....gtttccataggctccattag 1191

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1191	100.0	1191	6	BD144298	BD144298 Novel G-p
2	1191	100.0	1191	9	AB083586	AB083586 Homo sapi
3	1191	100.0	1493	9	AF237762	AF237762 Homo sapi
4	1191	100.0	1498	6	AR083245	AR083245 Sequence
5	1191	100.0	1535	9	BC020614	BC020614 Homo sapi
6	1191	100.0	1546	6	AX549299	AX549299 Sequence
7	1191	100.0	1546	9	AF282693	AF282693 Homo sapi
8	1191	100.0	1595	6	AX247564	AX247564 Sequence
9	1191	100.0	141003	9	AC078778	AC078778 Homo sapi
10	887.6	74.5	1574	10	BC023249	BC023249 Mus muscu
11	887.6	74.5	207421	2	AC021643	AC021643 Mus muscu
12	886	74.4	1611	10	AF272948	AF272948 Rattus no
13	867.8	72.9	244845	2	AC126846	AC126846 Homo sapi
14	707.6	59.4	141003	2	AC016463	BD229108 Endogeneo
15	87.8	7.4	1382	6	BD229108	AR431783 Sequence
16	87.8	7.4	1382	6	AR431783	AX549134 Sequence
17	87.8	7.4	1382	9	AF091890	AF091890 Homo sapi
18	87.8	7.4	1382	9	AF091890	AR044154 Sequence
19	87.8	7.4	1584	6	AR044154	AR269721 Sequence
20	87.8	7.4	1584	6	AR269721	BD007520 Novel his
21	87.8	7.4	1590	9	AY275468	AY275468 Homo sapi
22	87.8	7.4	2400	9	AK122656	AK122656 Homo sapi
23	87.8	7.4	2733	9	BC028163	BC028163 Homo sapi
24	87.8	7.3	2481	6	AR044088	AR044088 Sequence
25	87	7.3	2481	6	AR091709	AR091709 Sequence
26	87	7.3	2481	6	AX573819	AX573819 Sequence
27	87	7.3	2481	6	BD144779	BD144779 Adrenergi
28	87	7.2	1663	6	AX467017	AX467017 Sequence
29	86.2	7.0	1560	9	HUMALAR	L31773 Human alpha
30	83	7.0	1738	6	AR030766	AR030766 Sequence
31	83	7.0	1738	6	AR088757	AR088757 Sequence
32	83	7.0	1738	6	AR101770	AR101770 Sequence
33	83	7.0	1738	6	I26009	I26009 Sequence 3
34	83	7.0	1738	6	I30002	I30002 Sequence 3
35	83	7.0	1738	6	I83625	I83625 Sequence 3
36	83	7.0	1738	6	AR228241	AR228241 Sequence
37	83	7.0	1738	6	AR270839	AR270839 Sequence
38	83	7.0	1738	6	AR373863	AR373863 Sequence
39	83	7.0	1738	6	AX136023	AX136023 Sequence
40	83	7.0	1738	6	AX137520	AX137520 Sequence
41	83	7.0	1738	9	HSU03865	U03865 Human adren
42	83	7.0	1786	6	AX548750	AX548750 Sequence
43	83	7.0	2669	9	HUMADRENA	M99589 Homo sapien
44	83	7.0	8727	9	AC127458	AC127458 Homo sapi
45	83	7.0	8727	9	AC127458	

ALIGNMENTS

RESULT 1	BD144298	BD144298	1191 bp	DNA	linear	PAT 17-JAN-2003
LOCUS	BD144298	Novel G-protein coupled receptors.				
DEFINITION	BD144298	BD144298				
ACCESSION	BD144298.1	GI:27850056				
VERSION	JP 2002112793-A/23.					
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 1191)					
AUTHORS	Haga, T., Takeda, S. and Miyake, N.					
TITLE	Novel G-protein coupled receptors					
JOURNAL	Patent: JP 2002112793-A 23 16-APR-2002;					

Pred. No. is the number of results predicted by chance to have a

Query Match 100.0%; Score 1191; DB 9; Length 1493;
Best Local Similarity 100.0%; Pred. No. 1.2e-299;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 128

QY 61 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 120
Db TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 188

QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
Db ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 248

QY 181 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 240
Db AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 308

QY 241 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGAGGGTATTTGGGCTCTCCTT 300
Db TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGAGGGTATTTGGGCTCTCCTT 368

QY 301 TTGTCCTCAATTTCTGCTCCATCTGACCTGACCTCTGCTCATGCACTGGGACGCTACCTC 360
Db TTGTCCTCAATTTCTGCTCCATCTGACCTGACCTCTGCTCATGCACTGGGACGCTACCTC 428

QY 361 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 420
Db CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 488

QY 421 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 480
Db CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 548

QY 481 CTGGTACCTGTAGTCTGACCTGCACTGAGCTTTGACCGCATCCGAGGCGGCTTACACCACC 540
Db CTGGTACCTGTAGTCTGACCTGCACTGAGCTTTGACCGCATCCGAGGCGGCTTACACCACC 608

QY 541 ATCCTCATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
Db ATCCTCATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 668

QY 601 ATCCACGCCAGGTCAACAGAGCAGCACAGGCACCTGGACCAATACAAGTTGCGACAGGCA 660
Db ATCCACGCCAGGTCAACAGAGCAGCACAGGCACCTGGACCAATACAAGTTGCGACAGGCA 728

QY 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTTTCCAGGAG 720
Db AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTTTCCAGGAG 788

QY 721 CTGGACAGCAGGTTAGCATCAGAGGACCCAGTGAAGGATTTTCATCTGAGCCAGTCACT 780
Db CTGGACAGCAGGTTAGCATCAGAGGACCCAGTGAAGGATTTTCATCTGAGCCAGTCACT 848

QY 781 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 840
Db GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 908

QY 841 AAGAGAGCTAAGCAGATGGGAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGGCCA 900
Db AAGAGAGCTAAGCAGATGGGAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGGCCA 968

QY 901 ATTAAAGGAGCCAGAGAGCTCCGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db ATTAAAGGAGCCAGAGAGCTCCGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1028

QY 961 TGTGTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db TGTGTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1088

QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGTCACACCTCACCTGG 1080

Db 1089 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGTCACACCTCACCTGG 1148
QY 1081 CTCAATGTTGTCATCAACCTGTGCTCTATGAGCCATGAACCGCAATTCGCCAAGCA 1140
Db 1149 CTCAATGTTGTCATCAACCTGTGCTCTATGAGCCATGAACCGCAATTCGCCAAGCA 1208
QY 1141 TATGGCTCCATTTTAAAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1209 TATGGCTCCATTTTAAAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1259

RESULT 4
AR083245
LOCUS AR083245 1498 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 1 from patent US 5976834.
ACCESSION AR083245
VERSION AR083245.1 GI:10010035
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1498)
AUTHORS Sathre,G.Madhusudan., Fuetterer,W.S., Bergsma,D.John. and Ellis,C.
TITLE cDNA clone HNFJD15 that encodes a novel human 7-transmembrane receptor
JOURNAL Patent: US 5976834-A 1 02-NOV-1999;
FEATURES Location/Qualifiers
source 1..1498
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 1191; DB 6; Length 1498;
Best Local Similarity 100.0%; Pred. No. 1.2e-299;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db 76 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 135

QY 61 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 120
Db 136 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 195

QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
Db 196 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 255

QY 181 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTCAAGCCCTTCTCTGTGGACACC 240
Db 256 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTCAAGCCCTTCTCTGTGGACACC 315

QY 241 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGAGGGTATTTGGGCTCCTCCTT 300
Db 316 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGAGGGTATTTGGGCTCCTCCTT 375

QY 301 TTTGCTCCAAATTCTGTCTCCATCCTGACCCCTCTGCTCAGCCCTTCTGAGGGTATTTGGGCTCCTCCTT 360
Db 376 TTTGCTCCAAATTCTGTCTCCATCCTGACCCCTCTGCTCAGCCCTTCTGAGGGTATTTGGGCTCCTCCTT 435

QY 361 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 420
Db 436 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 495

QY 421 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTGTGCTCCCTCTGCGCTATTATATC 480
Db 496 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTGTGCTCCCTCTGCGCTATTATATC 555

QY 481 CTGGTACCTGTAGTCTGCACTGCACTTTTGACCGCATCCGAGGCGGCTTACACCACC 540
Db 556 CTGGTACCTGTAGTCTGCACTGCACTTTTGACCGCATCCGAGGCGGCTTACACCACC 615

QY 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
616 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 675
QY 601 ATCCACCGCCAGGTCAAAACGACGACGACAGGCACTGGACCAATACAAGTTGGACAGGCA 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
676 ATCCACCGCCAGGTCAAAACGACGACGACAGGCACTGGACCAATACAAGTTGGACAGGCA 735
QY 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCCTGGTCTGTTCCAGGAG 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
736 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCCTGGTCTGTTCCAGGAG 795
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTCATCTGAGCCAGTCAGT 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
796 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTCATCTGAGCCAGTCAGT 855
QY 781 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
856 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 915
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCCA 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
916 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCCA 975
QY 901 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
976 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1035
QY 961 TGTTTGTGTTGCTCTGCTTCCCTGCTTGCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1036 TGTTTGTGTTGCTCTGCTTCCCTGCTTGCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1095
QY 1021 CTGGATGCCAGAGTCCAGGTCCTCCGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1080
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1096 CTGGATGCCAGAGTCCAGGTCCTCCGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1155
QY 1081 CTCATGTTGTCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAAATCCGCAAGCA 1140
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1156 CTCATGTTGTCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAAATCCGCAAGCA 1215
QY 1141 TATGGCTCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1216 TATGGCTCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1266

RESULT 5
BC020614
LOCUS BC020614 1535 bp mRNA linear PRI 06-OCT-2003
DEFINITION Homo sapiens G protein-coupled receptor 84, mRNA (cDNA clone MGC:2224 IMAGE:4279185), complete cds.
ACCESSION BC020614 GI:18089044
VERSION BC020614.1
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1535)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1535)
Strausberg,R.
Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 35 Row: k Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9966838.
Location/Qualifiers
1. .1535

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:2224 IMAGE:4279185"
/tissue_type="Brain, primitive neuroectodermal"
/clone_lib="NIH MGC_56"
/lab_host="DH10B"
/note="Vector: pDNR-LIB"
1. .1535
/gene="GPR84"
/note="synonyms: EX33, GPCR4"
/db_xref="LocusID:53831"
/db_xref="MIM:606383"
101. .1291
/codon_start=1
/product="inflammation-related G protein-coupled receptor EX33"
/protein_id="AAH20614.1"
/db_xref="GI:18089045"
/db_xref="LocusID:53831"
/translation="MNSSDANFSCYHESVLGYRYVAVSWGVVAVTGVNVLTLA LAIQPKLRTFRNLLIANLTADLLYCTLLQPFSDTYLHLHWRGTATFCRVFGLLLFA SNSVSILTCLIALGRYLLIAHPKLFQVFSAGKTVLALVSTWVGVAFAFLWPIYI LVPVCTCSFDRIRGRPYTILMGIFYVLGLSSVGFYCLIHROVKRAAALDQYKLR QASIHNSHVARTDEAMPGRFQELDSRLASGGSPGISSEPVSAATTQTLEGDSSEVGD QINSKRAKQMAEKSPEASAKAQPIKGARRAPDSSEFGKVTMCFVFLCALSYP FLLNLILDARVQAPRVVHMLAANLTWNGCINPVLVAAAMNRQFRQAYGSILKGRPSF HRLH"

gene

CDS

misc_feature
323. .742
/note="7tm_1; Region: 7 transmembrane receptor (rhodopsin family)"
/db_xref="CDD:pfam00001"
1010. .1210
/note="7tm_1; Region: 7 transmembrane receptor (rhodopsin family)"
/db_xref="CDD:pfam00001"

misc_feature

ORIGIN

QY 481 CTGTACCTGTAGTCTGCACCTGCAGCTTTGACCGATCCGAGGCCGGCCTTACACCACC 540
|||||
Db 571 CTGTACCTGTAGTCTGCACCTGCAGCTTTGACCGATCCGAGGCCGGCCTTACACCACC 630
|||||
QY 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 600
|||||
Db 631 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 690
|||||
QY 601 ATCCACCGCCAGGTCAAAACGACGACGACAGGCACCTGGACCAATACAAGTTGGCAGAGCA 660
|||||
Db 691 ATCCACCGCCAGGTCAAAACGACGACGACAGGCACCTGGACCAATACAAGTTGGCAGAGCA 750
|||||
QY 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTTCCAGGAG 720
|||||
Db 751 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTTCCAGGAG 810
|||||
QY 721 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 780
|||||
Db 811 CTGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 870
|||||
QY 781 GCTGCCACCAACCCAGACCTTGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
|||||
Db 871 GCTGCCACCAACCCAGACCTTGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 930
|||||
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGGCCA 900
|||||
Db 931 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGGCCA 990
|||||
QY 901 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGTGAATG 960
|||||
Db 991 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGTGAATG 1050
|||||
QY 961 TGTGTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
|||||
Db 1051 TGTGTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1110
|||||
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGTCCACATGCTTGTGCCAACCTCACCTGG 1080
|||||
Db 1111 CTGGATGCCAGAGTCCAGGCTCCCGGGTGTCCACATGCTTGTGCCAACCTCACCTGG 1170
|||||
QY 1081 CTCAATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCGGCAAAGCA 1140
Db 1171 CTCAATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCGGCAAAGCA 1230
|||||
QY 1141 TATGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 1191
|||||
Db 1231 TATGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 1281
|||||
RESULT 7
AF282693
LOCUS AF282693 1546 bp mRNA linear PRI 23-SEP-2002
DEFINITION Homo sapiens inflammation-related G protein-coupled receptor EX33
(EX33) mRNA, complete cds.
ACCESSION AF282693
VERSION AF282693.1 GI:9652260
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1546)
AUTHORS Yousefi,S., Cooper,P.R., Potter,S.L., Mueck,B. and Jarai,G.
TITLE Cloning and expression analysis of a novel G-protein-coupled
receptor selectively expressed on granulocytes
J. Leukoc. Biol. 69 (6), 1045-1052 (2001)
JOURNAL 21297471
MEDLINE 11404393
PUBMED
REFERENCE 2 (bases 1 to 1546)
AUTHORS Yousefi,S., Cooper,P., Mueck,B., Potter,S. and Jarai,G.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-2000) NHRC, Wimblehurst, Horsham, West Sussex
RH12 5AB, UK

FEATURES
source
Location/Qualifiers
1..1546
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..1546
/gene="EX33"
91..1281
/gene="EX33"
/codon_start=1
/product="inflammation-related G protein-coupled receptor
EX33"
/protein_id="AAF91467.1"
/db_xref="GI:9652261"
/translation="MNSSDANFSCYHESVLGYRVAVSWGVVAVTGTGNNVLTLLA
LAIQPKLRTFRNLLIANLTLADLLYCTLLQPFSDVDTYHLHWRTGATFCRVFGLLFA
SNSVILTLCLIALGRYLLIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYI
LVPVCTCSFDRIRGRPYTILMGIYFVLGSSVGIIFYCLIHQVKRAAQLDQYKLR
QASIHSHVARTDEAMPGRFQELDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGD
QINSKRAKQMAEKSPPEASAKAQPIKGARRAPDSSEFQKVTMCFVFLCFALSYIP
FLLNLILDARVQAPRVVHMLAANLTWLNGCINPVIYAAMNRQFRQAYGSIILKGRPSF
HRLH"
ORIGIN
Query Match 100.0%; Score 1191; DB 9; Length 1546;
Best local Similarity 100.0%; Pred. No. 1.2e-299;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTCTGGGCTATCGT 60
|||||
Db 91 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTCTGGGCTATCGT 150
|||||
QY 61 TATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC 120
|||||
Db 151 TATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC 210
|||||
QY 121 ACCCTACTGGCCTTGGCCATCCAGCCAAAGTCCGTACCCGATTCAACCTGCTCATAGCC 180
|||||
Db 211 ACCCTACTGGCCTTGGCCATCCAGCCAAAGTCCGTACCCGATTCAACCTGCTCATAGCC 270
|||||
QY 181 AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC 240
|||||
Db 271 AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC 330
|||||
QY 241 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGCAGGATATTGGGCTCCTCCTT 300
Db 331 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGCAGGATATTGGGCTCCTCCTT 390
|||||
QY 301 TTTGCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGACGCTACCTC 360
Db 391 TTTGCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGACGCTACCTC 450
|||||
QY 361 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 420
Db 451 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 510
|||||
QY 421 CTGGTGAGCACCTGGGTTGTGGGGGTGGCCAGCTTTGCTCCCTCTTGGCCTATTATATC 480
Db 511 CTGGTGAGCACCTGGGTTGTGGGGGTGGCCAGCTTTGCTCCCTCTTGGCCTATTATATC 570
|||||
QY 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCCGCATCCGAGGCCCGCCTTACACCACC 540
Db 571 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCCGCATCCGAGGCCCGCCTTACACCACC 630
|||||
QY 541 ATCCTCATGGGCATCTACTTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCCTC 600
Db 631 ATCCTCATGGGCATCTACTTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCCTC 690
|||||
QY 601 ATCCACCGCCAGGTCAAAACGACGACGACGACCTGGACCAATACAAGTTGCGACAGGCA 660
Db 691 ATCCACCGCCAGGTCAAAACGACGACGACGACCTGGACCAATACAAGTTGCGACAGGCA 750
|||||
QY 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTTCCAGGAG 720

Db 751 AGCATCCACTCAACCATGTGGCAGGACTGATGAGGCCATGCTGGTCTTCAGGAG 810
Qy 721 CTGGACAGCAGGTTAGCATCAGGAGACCCAGTGGGGAATTCATCTGAGCCAGTCA 780
Db 811 CTGGACAGCAGGTTAGCATCAGGAGACCCAGTGGGGAATTCATCTGAGCCAGTCA 870
Qy 781 GCTGCCACACCCAGACCCCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 840
Db 871 GCTGCCACACCCAGACCCCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 930
Qy 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCA 900
Db 931 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCA 990
Qy 901 ATTAAGAGAGCCAGAGACTCCGGATTTCTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 991 ATTAAGAGAGCCAGAGACTCCGGATTTCTCATCGGAATTTGGGAAGGTGACTCGAATG 1050
Qy 961 TGTCTTGTCTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTCTGCTCAACATT 1020
Db 1051 TGTCTTGTCTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTCTGCTCAACATT 1110
Qy 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGTTGCTGCCAACCTCACCTGG 1080
Db 1111 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGTTGCTGCCAACCTCACCTGG 1170
Qy 1081 CTCAATGGTGTGCATCAACCTGTGCTCTATGCAGCCATGAACCCCAATTCGCGCAAGCA 1140
Db 1171 CTCAATGGTGTGCATCAACCTGTGCTCTATGCAGCCATGAACCCCAATTCGCGCAAGCA 1230
Qy 1141 TATGGTCCATTTTAAAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1231 TATGGTCCATTTTAAAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1281

RESULT 8
LOCUS AX247564 1595 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1 from Patent WO0166597.
ACCESSION AX247564
VERSION AX247564.1 GI:15862254

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Jarai, G., Cooper, P.R. and Yousefi, S.
TITLE Inflammation-related gene
JOURNAL Patent: WO 0166597-A 1 13-SEP-2001;
FEATURES Location/Qualifiers
source 1..1595
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 1191; DB 6; Length 1595;
Best Local Similarity 100.0%; Pred. No. 1.2e-299;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGGAAAGAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGTATCGT 60
Db 140 ATGTGGAAAGAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGTATCGT 199
Qy 61 TATGTTGAGTTAGTGGGGGTGGTGGTGTGTGACAGCACCGTGGGCAATGTGCTC 120
Db 200 TATGTTGAGTTAGTGGGGGTGGTGGTGTGTGACAGCACCGTGGGCAATGTGCTC 259
Qy 121 ACCCTACTGGCTTGGCCATCCAGCCAAAGCTCCGTACCGATTCAACCTGCTCATAGCC 180
Db 260 ACCCTACTGGCTTGGCCATCCAGCCAAAGCTCCGTACCGATTCAACCTGCTCATAGCC 319

Qy 181 AACCTCAGACTGGCTGATCTCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC 240
Db 320 AACCTCAGACTGGCTGATCTCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC 379
Qy 241 TACCTCCACCTGCACCTGGCGACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCTCTCCT 300
Db 380 TACCTCCACCTGCACCTGGCGACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCTCTCCT 439
Qy 301 TTTGCCCTCCAATTTCTGTCTCCATCTGACCTCTGCTCATCGCACTGGGACGTACCTC 360
Db 440 TTTGCCCTCCAATTTCTGTCTCCATCTGACCTCTGCTCATCGCACTGGGACGTACCTC 499
Qy 361 CTCATTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCACCAAGGGGATAGTGTGGCA 420
Db 500 CTCATTGCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCACCAAGGGGATAGTGTGGCA 559
Qy 421 CTGGTGCACACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTTATATC 480
Db 560 CTGGTGCACACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTTATATC 619
Qy 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCGCGCTTACACCAAC 540
Db 620 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCGCGCTTACACCAAC 679
Qy 541 ATCCTCATGGGCATCTACTTTGTGCTTGGCTCAGCAGTGTGGCATCTTCTATTTGCTC 600
Db 680 ATCCTCATGGGCATCTACTTTGTGCTTGGCTCAGCAGTGTGGCATCTTCTATTTGCTC 739
Qy 601 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCAATACAAGTTGCGACAGGCA 660
Db 740 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCAATACAAGTTGCGACAGGCA 799
Qy 661 AGCATCCACTCCAACCATGTGSCCAGGACTGATGAGGCCATGCTGCTGTTCCAGGAG 720
Db 800 AGCATCCACTCCAACCATGTGSCCAGGACTGATGAGGCCATGCTGCTGTTCCAGGAG 859
Qy 721 CTGGACAGCAGGTTAGCATCAGGAGACCCAGTGGGGGATTTTCATCTGAGCCAGTCA 780
Db 860 CTGGACAGCAGGTTAGCATCAGGAGACCCAGTGGGGGATTTTCATCTGAGCCAGTCA 919
Qy 781 GCTGCCACACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 840
Db 920 GCTGCCACACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 979
Qy 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCA 900
Db 980 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCA 1039
Qy 901 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 1040 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1099
Qy 961 TGTCTTGTGTTCTCTGCTTGTGCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1020
Db 1100 TGTCTTGTGTTCTCTGCTTGTGCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1159
Qy 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCATGCTGCTGCCAACCTCACTGG 1080
Db 1160 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCATGCTGCTGCCAACCTCACTGG 1219
Qy 1081 CTCAATGTTGTCATCAACCTCTGCTCTATGCAGCCATGAACCGCAATTCGCGCAAGCA 1140
Db 1220 CTCAATGTTGTCATCAACCTCTGCTCTATGCAGCCATGAACCGCAATTCGCGCAAGCA 1279
Qy 1141 TATGGTCCATTTTAAAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1280 TATGGTCCATTTTAAAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1330

RESULT 9
AC078778
LOCUS AC078778 141003 bp DNA linear PRI 21-FEB-2003

DEFINITION Homo sapiens 12 BAC RP11-968A15 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
AC078778
VERSION AC078778.34 GI:23307958
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 141003)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Dearthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Ednhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S.,
Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P.,
Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N.,
Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P.,
Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M.,
Holloway,C., Hollins,B., Homsy,F., Howard,S., Huber,J., Hulyk,S.,
Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y.,
Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U.,
King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N.,
Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O.,
Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X.,
Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P.,
Marandel,I., Martin,R., Martindale,A., Martinez,E., Massey,E.,
Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S.,
Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T.,
Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M.,
Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shim,C., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 141003)
Worley,K.C.
Direct Submission
TITLE Submitted (03-AUG-2000) Human Genome Sequencing Center, Department
JOURNAL of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 141003)
Worley,K.C.
Direct Submission
TITLE Submitted (27-AUG-2002) Human Genome Sequencing Center, Department
JOURNAL of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 141003)
Worley,K.C.
Direct Submission
TITLE Submitted (25-SEP-2002) Human Genome Sequencing Center, Department
JOURNAL of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 141003)

AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT On Sep 25, 2002 this sequence version replaced gi:22477001.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STSS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
<http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht>
ml.

FEATURES
source Location/Qualifiers
1. 141003
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-968A15"
complement(1..2005)
/note="overlaps bases 1..2005 of clone AC079313"
/function="clone overlap"
460..659
/standard_name="RH158"
18075..18234
/standard_name="NIB1371"
1811..18242
/standard_name="A002C47"
18229..18400
/standard_name="RH78595"
18349..18457
/standard_name="D12S1927"
19062..19158
/standard_name="Bdya3g12"
71395..71512
/standard_name="D11S2560"
77459..77710
/standard_name="WI-7866"
77500..77704
/standard_name="RH44735"
84170..84320
/standard_name="D12S1994"

misc_feature
STS
STS
STS
STS
STS
STS
STS
STS
STS
STS

JOURNAL human and mouse cDNA sequences
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 22388257
2 (bases 1 to 1574)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 40 Row: 0 Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 13507671.

FEATURES

source

1. .1574
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="MGC:30824 IMAGE:3995193"
/tissue_type="Mammary tumor metastatized to lung. Tumor
arose spontaneously from a senescent normal mammary
(clonal) outgrowth infected with the virus MMV."
/clone_lib="NCI CGAP_Lu29"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

gene

1. .1574
/gene="Gpr84"
/note="synonym: EX33"
/db_xref="LocusID:80910"
/db_xref="MGI:1934129"
147. .1337
/codon_start=1
/product="G protein-coupled receptor 84"
/protein_id="AAH23249.1"
/db_xref="GI:23273890"
/db_xref="LocusID:80910"

CDS

/translation="MNSSDANFSCYHESVLGYRPAVINGVAVAVTGVGNVLTLLA
LAIRPKLRTFRNLLIANLTADLLYCTLLQPFSDTYLHLHWRGTGAVFCRIFGLLLFT
SNSVSLTLCLIALGRYLTAHPKLPQVFSAGKIVLALVGSWVGVSFAPLWNVFV
LVPVCTCSFDRMRGRPYTILMGIYFVLGLSSVGVFCLIHQVRAARALDQYGLH
QASIRSHQVAGTQEAHPGHFQELDSGVASRGPSSEGISSEPVSAATTOTLEGDSSEAGG
QGIRKAAQQAIAERSLPEVHRKPRETAGARRATAPSEFGKVTMCFPVFLCFALSYIP
FLLNLILDARGAPRVVHVMVAANLTWLNINCINPVLVYAMNRQFRHAYGSILKRGPPQSF
RRFH"

misc_feature

369. .818
/note="7tm_1; Region: 7 transmembrane receptor (rhodopsin
family)"
/db_xref="CDD:pfam00001"

misc_feature

1032. .1256
/note="7tm_1; Region: 7 transmembrane receptor (rhodopsin
family)"
/db_xref="CDD:pfam00001"

ORIGIN

Query Match 74.5%; Score 887.6; DB 10; Length 1574;
Best Local Similarity 84.1%; Pred. No. 1.8e-220;
Matches 1001; Conservative 0; Mismatches 189; Indels 0; Gaps 0;
QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
DB 147 ATGTGGAACAGCTCAGATGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGA 206
QY 61 TATGTTGAGTTAGCTGGGGGTTGGTGTGTGACAGGACCCGTGGGCAATGTGCTC 120
DB 207 TACTTTGAGTTATCTGGGGGTTGGCAGTGGCTGTGACAGGACGGTGGCAATGTGCTC 266
QY 121 ACCCTACTGGCCCTTGGCCATCCAGCCCAAGCTCCGTACCCGANTCAACCTGCTCATAGCC 180
DB 267 ACTCTGTGGCCTTGGCCATTGCTCCCAAGCTCCGAACCCGTTCAACCTGCTCATAGCC 326
QY 181 AACCTCACACTGGCTGATCTCTCTACTGTCACGCTCCCTTTCAGGCCCTTCTCTGTGGACACC 240
DB 327 AACCTCACCTGGCTGATCTACTTACTGTCACGCTCCCTGACGCTTCTCCGTGGACACA 386
QY 241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGTATTTGGGCTCCTCCTT 300
DB 387 TACCTCCACCTGCACTGGCGGTACCGCGGGTCTTCTGTAGAATATTTGGACTCCTCCTC 446
QY 301 TTTGCTCCAAATTTCTGTCTCCATCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 360
DB 447 TTTACTTCCAAATTTCTGTCTCCATCTGACCCCTCTGTCTCATTTGCTTAGGACGCTACCTC 506
QY 361 CTCATTGCCCAACCTTAAGCTTTTTCCTCCCAAGTTTTCAGTGCCCAAGGGGATAGTCTGGCA 420
DB 507 CTCATTGCCCAACCTTAAGCTTTTTCCTCCAGTTTTCAGTGCCCAAGGGGATCGTCTGGCA 566
QY 421 CTGGTGAGCACCTGGTTGTGGGGCTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 480
DB 567 CTGGTGAGCACCTGGTTGTGGGGGTGACCAAGCTTTGCCCCCTCTGGAATGTTTTTGTG 626
QY 481 CTGGTACCTGTAGTCTGCACCTGCACTTTGACCGCATCCGAGCGCGGCTTACACCAACC 540
DB 627 TTGGTGCCAGTTGTCTGCACCTGCACTTTGACCGCATCGGAGCGCGGCTTACACCAACC 686
QY 541 ATCTCTATGGGCATCTACTTTGTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCTC 600
DB 687 ATCTCTATGGGCATCTACTTTGTTGCTTGGGCTCAGCAGCGTGGGCTCTTCTACTGCTC 746
QY 601 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 660
DB 747 ATCCACCGCCAGGTGAAGCGTGGGCTCGGCTCGAGCACTGGACCAATACGGGCTGCATCAGGCC 806
QY 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTGTTTCCAGGAG 720
DB 807 AGCATCCGCTCTCATCAGGTGGTGGGACACAAGAGCCATGCCTGGCCACTTCCAGGAG 866
QY 721 CTGGACAGCAGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCACTGTAGCCAGTCAGT 780
DB 867 CTAGACAGCGGGGTGCTCAAGAGGGGCCAGCGAGGGGATTTCATCTGAGCCAGTCAGT 926
QY 781 GCTGCCACCACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 840
DB 927 GCTGCGACCACGACACCCCTGGAAGGTGATTGTCGTCGGAAGCTGGGGGCCAGGGCATTAGA 986
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAAGCCAGCCA 900
DB 987 AAGGCAGCTCAACAGATCGCAGAGAGAGCCCTCCAGAAAGTGCATCGCAAGCCCGGGAA 1046
QY 901 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
DB 1047 ACTGCAGGAGCTCGCAGAGCCACAGATGCCCATCAGAGTTGCGGGAAGGTGACCCGATG 1106
QY 961 TGTTTGTGTTCTCTGCTTTTGGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
DB 1107 TGCTTCGAGTGTCTCTGCTTTCGCCCCTCAGCTACATCCCTTCTCTGTTGCTCAACATT 1166
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTCTGCCAACCTCACCTGG 1080

Db 1167 CTGGACGCCAGGGCGTCTCCACGAGTAGTCACATGGTGGTGCCAACTCACTGG 1226
QY 1081 CTCAATGGTTGATCAACCTGTGCTATGCGAGCCATGAACCGCAATTCGCCAAGCA 1140
Db 1227 CTCAACAGCTGATCAACCTGTGCTATGCGAGCCATGAACCGCAGTTTCGCCACGG 1286
QY 1141 TATGGCTCCATTTAAAGAGGGCCCGAGTTTCCATAGGTCCATTA 1190
Db 1287 TATGGCTCCATCTGAAACGCGGGCCACAGAGTTTCGCCCGGTCCATTA 1336

RESULT 11
AC021643
LOCUS AC021643 207421 bp DNA linear HTG 15-MAY-2002
DEFINITION Mus musculus chromosome 15 clone RP23-169K7 strain C57BL6/J,
WORKING DRAFT SEQUENCE, 23 unordered pieces.

ACCESSION AC021643
VERSION AC021643.12 GI:15143422
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 207421)
Grills, G., Han, J., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M.
Ioshikhes, I. P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M.
and Kucherlapati, R.

TITLE High Throughput Mouse Sequencing

JOURNAL Unpublished

REFERENCE 2

(bases 1 to 207421)
Grills, G., Han, J., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M.
Ioshikhes, I. P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M.
and Kucherlapati, R.

TITLE Direct Submission

JOURNAL Submitted

(19-JAN-2000) Department of Molecular Genetics, Albert
Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
Bronx, NY 10461, USA

COMMENT

On Aug 9, 2001 this sequence version replaced gi:14717145.

-----Genome Center

Center: Harvard Partners Genome Center

Center Code: HPGC

Web site: <http://www.hpcgg.org/Sequence/mouse.html>

Contact: hpgc@mdel.mgh.harvard.edu

-----Summary Statistics

Center project name: AAT

Sequencing vector: pUC18; L08752

Chemistry: Dye-terminator Big Dye; 100%

*Consensus quality: 193187 at least Q20

*Consensus quality: 190826 at least Q30

*Consensus quality: 186718 at least Q40

Estimated insert size: agarose-FP - N/A

*Estimated insert size: 206981 - sum-of-contigs

Quality coverage: agarose-FP - N/A

Quality coverage: 6.5 x in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 38304: contig of 38304 bp in length
* 38305 38324: gap of unknown length
* 38325 68273: contig of 29949 bp in length
* 68274 68293: gap of unknown length
* 68294 89009: contig of 20716 bp in length
* 89010 89029: gap of unknown length
* 89030 108492: contig of 19463 bp in length
* 108493 108512: gap of unknown length
* 108513 120232: contig of 11720 bp in length

* 120233 120252: gap of unknown length
* 120253 131080: contig of 10828 bp in length
* 131081 131100: gap of unknown length
* 131101 142689: contig of 11589 bp in length
* 142690 142709: gap of unknown length
* 142710 155481: contig of 12772 bp in length
* 155482 155501: gap of unknown length
* 155502 164014: contig of 8513 bp in length
* 164015 164034: gap of unknown length
* 164035 171335: contig of 7301 bp in length
* 171336 171355: gap of unknown length
* 171356 179422: contig of 8067 bp in length
* 179423 179442: gap of unknown length
* 179443 185328: contig of 5886 bp in length
* 185329 185348: gap of unknown length
* 185349 190531: contig of 5183 bp in length
* 190532 190551: gap of unknown length
* 190552 196001: contig of 5450 bp in length
* 196002 196021: gap of unknown length
* 196022 200348: contig of 4327 bp in length
* 200349 200368: gap of unknown length
* 200369 202575: contig of 2207 bp in length
* 202576 202595: gap of unknown length
* 202596 203643: contig of 1048 bp in length
* 203644 203663: gap of unknown length
* 203664 204541: contig of 878 bp in length
* 204542 204561: gap of unknown length
* 204562 204816: contig of 255 bp in length
* 204817 204836: gap of unknown length
* 204837 204909: contig of 73 bp in length
* 204910 204929: gap of unknown length
* 204930 206958: contig of 2029 bp in length
* 206959 206978: gap of unknown length
* 206979 207177: contig of 199 bp in length
* 207178 207197: gap of unknown length
* 207198 207421: contig of 224 bp in length.

FEATURES

source

1. 207421
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL6/J"
/db_xref="taxon:10090"
/chromosome="15"
/clone="RP23-169K7"
/sex="male"
misc_feature
1. 38304
/note="assembly_name:Contig87"
misc_feature
38325. 68273
/note="assembly_name:Contig86"
misc_feature
68294. 89009
/note="assembly_name:Contig85"
misc_feature
89030. 108492
/note="assembly_name:Contig84"
misc_feature
108513. 120232
/note="assembly_name:Contig83"
misc_feature
120253. 131080
/note="assembly_name:Contig82"
misc_feature
131101. 142689
/note="assembly_name:Contig81"
misc_feature
142710. 155481
/note="assembly_name:Contig80"
misc_feature
155502. 164014
/note="assembly_name:Contig79"
misc_feature
164035. 171335
/note="assembly_name:Contig78
clone_end:SP6
vector_side:right"
misc_feature
171356. 179422
/note="assembly_name:Contig77"
misc_feature
179443. 185328
/note="assembly_name:Contig76"
misc_feature
185349. 190531
/note="assembly_name:Contig75"

Qy	721	CTGGACAGCAGCTTAGCATCAGGAGGACCCAGT	GAGGGATTTTCATCTGAGCCAGTCAGT	780
Db	126812	CTAGACAGCGGGGTTCCTCAAGAGGGCCACG	GAGGGATTTTCATCTGAGCCAGTCAGT	126871
Qy	781	GCTGCCACCCAGACCCCTGGAAAGGGACTCAT	CAGAACTGGGAGACCAGATCAACAGC	840
Db	126872	GCTGCGACCAACGACACCTGGAAAGGTGATT	CGTCAGAACTGGGGCCAGGGCATTAGA	126931
Qy	841	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCT	CCAGAAAGCATCTGCCAAAGCCAGCCCA	900
Db	126932	AAGGCAGCTCAACAGATCGCAGAGAAAGCCCT	CCAGAAAGTCATCGCAAGCCCGGGAA	126991
Qy	901	ATTAAGGAGCCAGAAAGAGCTCCGGATTCTTC	ATCGGAAATTTGGGAAGTGACTCGAATG	960
Db	126992	ACTGCAGGAGCTCGCAGAGCCACAGATGCCCAT	CAGAGTTCGGGAAGTGACCCGTATG	127051
Qy	961	TGTTTTGCTGTCTTCTGTCTTTGCCCTGAGCT	ACATCCCTTCTTGTGCTCAACATT	1020
Db	127052	TGCTTCGAGTGTTCCTCTGTCTTCGCCCTCAG	CTACATCCCTTCTGTGCTCAACATT	127111
Qy	1021	CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCC	ACATGCTTGTGCTGCCAACCTCACCTGG	1080
Db	127112	CTGGACGCCAGGGCCGTCGTCCACAGTAGTGCA	CATGGTGGCTGCCAACCTCACCTGG	127171
Qy	1081	CTCAATGGTTGCATCAACCCCTGTGCTCTATGC	AGCCATGAACCGCCCAATTCGCCCAAGCA	1140
Db	127172	CTCAACAGCTGCATCAACCCCTGTGCTCTATGC	AGCCATGAACCGCCCAATTCGCCCAAGCA	127231
Qy	1141	TATGGCTCCATTTTAAAAAGAGGGCCCGGAGTT	TCCATAGGCTCCATTA	1190
Db	127232	TATGGCTCCATCTGAAACCGGGGCCACAGAGTT	TCCCGCGGTTCCATTA	127281

LOCUS	AF272948	1611 bp	mRNA	linear	ROD 06-APR-2001
DEFINITION	Mus musculus orphan G protein-coupled receptor 84 (Gpr84) mRNA,				

ACCESSION AF272948

KEYWORDS

ORGANISM

AUTHORS

MEDLINE

REFERENCE

TTTTT.F

PHOTOS

SECRET

STRA

3

/translation="MNSSDANFSCYHESVLYGYRFAIINGVAVAVTGTGVNLTLLA
LAIRPKLRTFRNFLLIADLLYCTLLQPFSDVDTYHLHWRGTGAVFCRIFGLLFT
SNSVSLTLCLIALGRYLLIAHPLFPQVFSAGKIVLALVGSWVGVTSFAPLWNVFE
LVPVCTCSFDMRGRPYTTILMGIYFVLGSSVGFYLIHQVKAARALDQYGLH
QASIRHQVAGTQEAMPGHFQELDSVASRGPSEGISSEPVSAATTQTLEGSSAEGG
QGIRKAAQIAERSLPEVHRKPRETAGARRATDAPSEFGKTRMCFVAFVLCFALSYP
FLLNLILDARAPRVVHMVAANLTWLNSCINPVLVYAMNRQFRHAYGSILKRPQSF
RRFH"

ORIGIN

Query Match	74.4%;	Score	886;	DB	10;	Length	1611;
Best Local Similarity	84.0%;	Pred.	No. 4.8e-220;				
Matches	1000;	Conservative	0;	Mismatches	190;	Indels	0;
Gaps	0;						
QY	1	ATGTGGAACAGCTGTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT	60				
Db	138	ATGTGGAACAGCTCAGATGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGCTATCGA	197				
QY	61	TATGTTGCAGTTAGTGGGGGTGGTGGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC	120				
Db	198	TACTTTGCAATTATCTGGGGCGTGGCAGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC	257				
QY	121	ACCCTACTGGCTGGCCATCCAGCCCAAGTCCGTACCCGATTCAACCTGCTCATAGCC	180				
Db	258	ACTCTGTGGCCTTGGCCATTCTGTCCTGCTACCATGAGTCTGTGCTGGCTATCGT	317				
QY	181	AACCTCACACTGGCTGATCTCTCTACTGACAGCTCCTTTCAGCCCTTCTCTGTGGACACC	240				
Db	318	AACCTCACCTGGCTGATCTACTCTACTGACAGCTCCTGACGCTTCTCTCGTGGACACA	377				
QY	241	TACCTCCACCTGCAGTGGCGCACCGGTGCCACCTTCTGACGGTATTTGGCTCCTCCTT	300				
Db	378	TACCTCCACCTCCATTGGCGTACCGGCGGTCTTCTGTAGAAATTTGGACTCCTCCTC	437				
QY	301	TTTGCCTCCAAATCTGTCTCCATCTCTGACCTCTGCTCATCGCACTGGGACGCTACCTC	360				
Db	438	TTTACTTCCAATCTGTCTCCATCTCTCACCTCTGTCTCATTTGCTTAGGACGCTACCTC	497				
QY	361	CTCATTGCCCCACCTAAGCTTTTTCCTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGSCA	420				
Db	498	CTCATTGCCCCACCTAAGCTCTTTCCCAAGTTTTCAGTGCCCAAGGGATCGTGTGSCA	557				
QY	421	CTGGTGAGCACCTGGGTTGTGGCGTGGCAGCTTTGCTCCCTCTGGCCCTATTATATC	480				
Db	558	CTGGTGAGCACCTGGGTTGTGGCGTGGCAGCTTTGCTCCCTCTGGCCCTATTATATC	617				
QY	481	CTGGTACCTGTAGTCTGCACCTGCAGCTTGACCGCATCCGAGCGCGGCTTACACCACC	540				
Db	618	TTGGTGCCAGTTGTCTGCACCTTGACAGCTTTGACCGCATGCGAGCGCGGCTTACACCACC	677				
QY	541	ATCCTCATGGGCATCTACTTTGTGCTTGGCTCAGCAGTGTGGCATCTTCTATTGCTC	600				
Db	678	ATCCTCATGGGCATCTACTTTGTGCTTGGCTCAGCAGTGTGGCGTCTTCTACTGCTC	737				
QY	601	ATCCACCGCCAGGTCAAACGAGCAGCAGCAGCTGGACCAATACAAAGTTGGCAGGCA	660				
Db	738	ATCCACCGCCAGGTCAAACGAGTGGCTCGAGCACTGGACCAATACCGGCTGCATCAGGCC	797				
QY	661	AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGTTTCCAGGAG	720				
Db	798	AGCATCCGCTCTCATCAGGTGGCTGGGACACAAGAAGCCATGCTGCTGCTTCCAGGAG	857				
QY	721	CTGGACAGCAGGTAGCATCAGGAGGACCCAGTGGGGATTTCTATCTGAGCCAGTCACT	780				
Db	858	CTAGACAGCGGGTGTCTCAAGAGGGCCCGAGGGGATTTCTATCTGAGCCAGTCACT	917				
QY	781	GCTGCCACCCAGCACCTGGAAGGGGACTCATCAGAAGTGGGAGACCCAGATCAACAGC	840				
Db	918	GCTGCGACCCAGCAGACCTTGAAGGTGATTCGTGAGAAGCTGGGGGCCAGGGCATTAGA	977				
QY	841	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA	900				
Db	978	AAGGCAGCTCAACAGATCGCAGAGAGAGGCTTCCAGAAGTGCATCGCAAGCCCGGGAA	1037				

QY	901	ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	960
Db	1038	ACTGAGGAGCTCCAGAGCCACAGATGCCCATCAGAGTTCCGGAAGGTGACCCGTATG	1097
QY	961	TGTTTTGCTGTCTCTCTGCTTTGCTGCTGAGCTACATCCCTTCTGCTGCTCAACATT	1020
Db	1098	TGCTTCGAGTGTCTCTCTGCTTCGCCCTCAGCTACATCCCTTCTGCTGCTCAACATT	1157
QY	1021	CTGGATGCCAGATCCAGGCTCCCGGGTGGTCCACATGCTTGTGTCACACCTCACCTGG	1080
Db	1158	CTGGACGCCAGGGCCGTGCTCCACGAGTAGTGCACATGGTGGTGCACACCTCACCTGG	1217
QY	1081	CTCAATGGTTGCATCAACCTGTGCTCTATGTCAGCCATGAACCGCAATTCGCCAAGCA	1140
Db	1218	CTCAACAGCTGCATCAACCTGTGCTCTATGTCAGCCATGAACCGCAGTTTCGCCACGG	1277
QY	1141	TATGGCTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTA	1190
Db	1278	TATGGCTCCATCTCTGAAACGGGGCCACAGAGTTTCGCCCGGTTCCATTA	1327

RESULT 13

AC126846	LOCUS	AC126846	244845 bp	DNA	linear	HTG 03-OCT-2002
DEFINITION	Rattus norvegicus clone CH230-11M7, *** SEQUENCING IN PROGRESS ***.					
ACCESSION	AC126846					
VERSION	HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_ENRICHED.					
KEYWORDS	Rattus norvegicus (Norway rat)					
SOURCE	Rattus norvegicus					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					

REFERENCE

AUTHORS	1 (bases 1 to 244845)
	Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Hui, Y., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseghe, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokeme, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L. L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,

Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wlarczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

TITLE

Direct Submission

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 244845)

AUTHORS

Worley,K.C.

TITLE

Direct Submission

JOURNAL

Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

REFERENCE

3 (bases 1 to 244845)

AUTHORS

Rat Genome Sequencing Consortium.

TITLE

Direct Submission

JOURNAL

Submitted (03-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Sep 10, 2002 this sequence version replaced gi:21722958.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only
contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GDTA

Center clone name: CH230-11M7

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 222716 bases at least Q40

Consensus quality: 225022 bases at least Q30

Consensus quality: 226487 bases at least Q20

Estimated insert size: 247241; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 244845: contig of 244845 bp in length.

FEATURES

source

Location/Qualifiers

1. .244845

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-11M7"

1. .1278

/note="wgs_contig"

1329. .2694

/note="wgs_contig"

239866. .241111

/note="wgs_contig"

misc_feature 243120..244845
/note="wgs_contig"

ORIGIN

Query Match 72.9%; Score 867.8; DB 2; Length 244845;

Best Local Similarity 83.0%; Pred. No. 2.4e-215;

Matches 989; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

QY	1	ATGTGGAACAGCTCTGACGGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT	60
DB	54676	ATGTGGAACAGCTCAGATGACAACTTCTCCTGCTACCATGAGTCTGTATGGGCTATCGA	54735
QY	61	TATGTTGCAGTTAGCTGGGGGGTGGTGGTGGCTGTGACAGGCACCGTGGCAATGTGCTC	120
DB	54736	TACTTTGCAGTTATCTGGGGCATGGTAGTGGCTGCAACAGGCACCGTGGCAATGTGCTC	54795
QY	121	ACCTACTGGCCTTGGCCCATCCAGCCCAAGTCCGTACCCGATTCAACCTGCTCATAGCC	180
DB	54796	ACCCTGTTGGCCTTGGCCCATCCGTCCCAAACTCCGAACCCGTTTCAACCTGCTCATG	54855
QY	181	AACCTCACACTGGGTGATCTCTCTACTGACGCTCCTTTCAGCCCTTCTCTGTGGACACC	240
DB	54856	AACCTCACCTGGGTGATCTACTCTACTGACGCTCCTGACGCTTCTCTCGTGGACACA	54915
QY	241	TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGTATTTGGGCTCCTCCTT	300
DB	54916	TACCTCCACCTCCATTGGCGCACCGCGGCCATCTTCTGTAGAATATTCGGACTCCTCCTC	54975
QY	301	TTTGCTTCCAATCTGTCTCCATCTGACCTCTGCCTCATCGCACTGG3ACGCTACCTC	360
DB	54976	TTTACTTCCAATCTGTCTCCATCTTACCCTCTGTCTCATTTGCTTAGGACGCTACCTT	55035
QY	361	CTCATTGCCCAACCTAAGCTTTTTCCTCCCAAGTTTTCAGTGCCAAGGGGATGCTGGCA	420
DB	55036	CTCATTGCCCAACCTAAGCTCTTTTCCCTCCAGGTTTTCAGTGCCAAGGGGATGCTGGCA	55095
QY	421	CTGGTGAGCACCTGGGTTGTGGGCGTGGCGCAGCTTGTCTCCCTCTGSCCTATTTATATC	480
DB	55096	CTAGTGGGCGAGCTGGGTTGTGGGCGTGGCGCAGCTTGTCCCTCTGGAATGTTATGTC	55155
QY	481	CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGGCCGCGCTTACACCACC	540
DB	55156	TTGGTGCCAGTTGTGACCTGCAGCTTTGACCGCGTGGAGGCCGCGCTTACACCACC	55215
QY	541	ATCCTCATGGGCGATCTACTTTGTGCTTGGGCTCAGCAGTGTGTCATCTTCTATTGCTC	600
DB	55216	ATCCTCATGGGCGATCTTCTTTGTGTTGGGCTCAGCAGCGTGGGCGCTTCTTACTGCTC	55275
QY	601	ATCCACCGCGAGGTCAAAACGAGCAGCAGCAGGCTGACCAATACAGTTGCGACAGGCA	660
DB	55276	ATCCACCGCGAGGTGAAGCGTGGGCTCGAGCGCTGGACAAATATGGGCTGCAGGAGGCC	55335
QY	661	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTGTTCCAGGAG	720
DB	55336	AGCATGCGCTCCCATCAGGTGTCTGGGACACATGAAGCTGTGCCAGGCCACTTCCAGGAG	55395
QY	721	CTGGACAGCAGGTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT	780
DB	55396	CTAGACAGCGGGCTTGCATCAAGAGGTCCAGCGAAGGGATTTTCATCTGAGCCAGTCAGT	55455
QY	781	GCTGCCACCAACCCAGACCTTGGAAAGGGGACTCATCAGAAAGTGGGAGACCATCAACAGC	840
DB	55456	GCTGCCAGCACACAGACCTTGGAAAGGTGATTCTGTGAGAGCGGGGACAGGGGCATGAGA	55515
QY	841	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCA	900
DB	55516	AAGGCAGCTCAGCAGATCTCAGAGAGAAAGCCCTCCAGAAAGTGCATCGCAAGACTGGAGGA	55575
QY	901	ATTAAAGGAGCCAGAAGAGCTCCGGATTCTTTCATCGGAATTTTGGGAAGTGAATGCGAATG	960
DB	55576	GCTGCAGGAGCACGAGAGCCACGGATGCACCATCGGAGTTCGGGAAGTGAATGCGGATG	55635
QY	961	TGTTTGTGTTCTCTGCTTTTGGCCTGAGCTACATCCCTTCTTGTGCTCAACATT	1020


```
Db      55636 TGCTTGCAGTGTCTTGGTTCCTTCGTCCTCAGCTACATCCCTTTCCTGCTGCTCAACATT 55695
QY      1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCACCTGG 1080
Db      55696 CTGGACGCCAGGCGCGCTCCACGAGTAGTGCATATGTTGTGCTGCCAACCTCACCTGG 55755
QY      1081 CTCAATGTTGCATCAACCTGTGCTCTATGTCAGCCATGAACCGCAATTCGCCCAAGCA 1140
Db      55756 CTCAACAGCTGCATCAACCTGTGCTCTATGTCAGCCATGAACCGCAGTTTCGCCAGGCT 55815
QY      1141 TATGGCTCCATTTTAAAGAGGCGCGCGCGAGTTTCCATAGGCTCCATTAG 1191
Db      55816 TATGGCTCCATCTCTGAAACGCGGGGCCACACAGTTTCCGACGGTTCATTAG 55866

RESULT 14
AC016463      141003 bp      DNA      linear      HTG 13-JUL-2000
LOCUS      Homo sapiens clone RP11-1009, LOW-PASS SEQUENCE SAMPLING.
DEFINITION      AC016463
ACCESSION      AC016463
VERSION      AC016463.3 GI:7144792
KEYWORDS      HTG; HTGS_PHASE0.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 141003)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-1009
Unpublished
2 (bases 1 to 141003)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:6910791.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3130
Center clone name: 10_O_9
-----
* NOTE: This record contains 152 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: September 23, 2004, 22:02:34 ; Search time 537.426 Seconds
(without alignments)
9414.519 Million cell updates/sec

Title: US-10-029-436-1_COPY_61_1251
Perfect score: 1191
Sequence: 1 atgtggaacagctctgagc.....gtttccataggctccattag 1191
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1191	100.0	1191	6	ABZ42892 Human GPC
2	1191	100.0	1227	6	Aai68793 Human MAR
3	1191	100.0	1311	8	Acc84331 Human hp1
4	1191	100.0	1498	2	Aav38513 Human 7-t
5	1191	100.0	1546	6	Aas98070 Human DNA
6	1191	100.0	1546	7	Abt17029 Human MP2
7	1191	100.0	1546	7	Abz42551 Human G p
8	1191	100.0	1579	4	Aai99548 Human exp
9	1191	100.0	1595	4	Aah78712 Human EX3
10	1191	100.0	2046	4	Aas28996 Genomic s
11	1191	100.0	2046	4	Aas30237 DNA encod
12	1191	100.0	2046	4	Aas35064 DNA #14 e
13	1191	100.0	2046	4	Aak77581 Human imm
14	1191	100.0	2046	4	Abz42551 Human gen
15	1191	100.0	2046	4	Abk44021 Genomic D
16	1191	100.0	2046	5	Aas29737 Human end
17	1191	100.0	2046	6	Abt07831 Novel hum
18	1191	100.0	2046	6	Abv84126 Human pol
19	1191	100.0	2046	7	Abv84126 Human gen
20	1191	100.0	2046	9	Adc46506 Human neo
21	1191	100.0	5460	6	Aai68792 Human MAR
22	1188	99.7	1188	7	Abv73365 Human TGR
23	1154.4	96.9	1416	4	Aak77579 Human imm

24	897.6	74.5	1191	7	ABV73374	Abv73374 Mouse TGR
25	840	70.5	840	6	AAS98133	Aas98133 Human DNA
26	684.6	57.5	712	4	AAK77580	Aak77580 Human imm
27	357.4	30.0	485	6	ABL89786	Ab189786 Human pol
28	346.2	29.1	347	4	AAK60376	Aak60376 Human imm
29	345.4	29.0	483	4	AAS28939	Aas28939 cDNA enco
30	345.4	29.0	483	4	AAS30167	Aas30167 DNA enco
31	345.4	29.0	483	4	AAS34782	Aas34782 cDNA enco
32	345.4	29.0	483	4	AAI99575	Aai99575 Human exp
33	345.4	29.0	483	4	ABA06396	Abz06396 Human cDN
34	345.4	29.0	483	4	ABK43453	Abk43453 DNA enco
35	345.4	29.0	483	5	AAS29521	Aas29521 Human end
36	345.4	29.0	483	6	ABT07774	Abt07774 Novel hum
37	345.4	29.0	483	6	ABV83733	Abv83733 Human pol
38	345.4	29.0	483	7	ACD01422	Ac01422 Human pol
39	345.4	29.0	483	9	ADC45940	Adc45940 Human neo
40	87.8	7.4	1382	3	AAZ51461	Aaz51461 Human G p
41	87.8	7.4	1382	7	ADA19230	Ada19230 Human ins
42	87.8	7.4	1382	7	ABZ42815	Abz42815 Human G p
43	87.8	7.4	1382	8	ADB67667	Adb67667 Human G-p
44	87.8	7.4	1584	2	AAV37701	Aav37701 Human his
45	87.8	7.4	1584	7	ACA55686	Aca55686 Signallin

ALIGNMENTS

RESULT 1
ABZ42892
ID ABZ42892 standard; DNA; 1191 BP.
XX
AC ABZ42892;
XX
DT 06-MAR-2003 (first entry)
XX
DE Human GPCR polynucleotide SEQ ID NO 45.
XX
KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
XX
OS drug development; gustatory; taste; fragrance; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200216548-A2.
XX
PD 28-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-IB001446.
XX
PR 04-AUG-2000; 2000JP-00237818.
PR 13-FEB-2001; 2001JP-00034434.
XX
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
Haga T, Takeda S, Mitaku S;
XX
WPI; 2002-304118/34.
DR P-PSDB; ABP95618.
XX
Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.
XX
PS Claim 9; SEQ ID NO 45; 97pp + Sequence Listing; Japanese.
XX
The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance

CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published pct sequences

Sequence 1191 BP; 242 A; 370 C; 294 G; 285 T; 0 U; 0 Other;

Query Match 100.0%; Score 1191; DB 6; Length 1191;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGTGGAACAGACTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT	60
Db	1	ATGTGGAACAGACTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT	60
QY	61	TATGTTGCAAGTTAGCTGGGGGGTGGTGGCTGTGACAGCACCGTGGGCAATGTGCTC	120
Db	61	TATGTTGCAAGTTAGCTGGGGGGTGGTGGCTGTGACAGCACCGTGGGCAATGTGCTC	120
QY	121	ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC	180
Db	121	ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC	180
QY	181	AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC	240
Db	181	AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC	240
QY	241	TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCT	300
Db	241	TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCT	300
QY	301	TTTGGCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC	360
Db	301	TTTGGCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC	360
QY	361	CTCATTTGCCACCCCTAAGCTTTTTCCTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGCTGGCA	420
Db	361	CTCATTTGCCACCCCTAAGCTTTTTCCTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGCTGGCA	420
QY	421	CTGGTGAGCACTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTCTGGCCTATTATATC	480
Db	421	CTGGTGAGCACTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTCTGGCCTATTATATC	480
QY	481	CTGGTACCTGTAGTCTGCACCTTGACCTTTTGACCGCATCCGAGGCCCGCCTTACACCACC	540
Db	481	CTGGTACCTGTAGTCTGCACCTTGACCTTTTGACCGCATCCGAGGCCCGCCTTACACCACC	540
QY	541	ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC	600
Db	541	ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC	600
QY	601	ATCCACCGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGCGACAGGCA	660
Db	601	ATCCACCGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGCGACAGGCA	660
QY	661	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGGCCATGCCTGCTTTCCAGGAG	720
Db	661	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGGCCATGCCTGCTTTCCAGGAG	720
QY	721	CTGGACAGCAGGTTAGCATCAGAGGACCCAGTGAAGGGGATTTTCATCTGAGCCAGTCACT	780
Db	721	CTGGACAGCAGGTTAGCATCAGAGGACCCAGTGAAGGGGATTTTCATCTGAGCCAGTCACT	780
QY	781	GCTGCCACCAACCCAGACCCCTGGAAAGGGGACTCATCAGAAGTGGGAGACAGATCAACAGC	840
Db	781	GCTGCCACCAACCCAGACCCCTGGAAAGGGGACTCATCAGAAGTGGGAGACAGATCAACAGC	840
QY	841	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA	900
Db	841	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA	900
QY	901	ATTAAAGGAGCCAGAAGAGCTCCGGATTCTTCATCGGAATTTTGGGAAGGTGACTCGAATG	960
Db	901	ATTAAAGGAGCCAGAAGAGCTCCGGATTCTTCATCGGAATTTTGGGAAGGTGACTCGAATG	960

RESULT 2.

AAI68793

AAI68793 standard; cDNA; 1227 BP.

AA
AC
AAI68793:XX
DT 22-JAN-2002 (first entry)

DE Human MAR1 cDNA fragment.

AA MAR1; monoamine receptor-1; human; cytostatic; gene therapy; tumour;
KW psychiatric disorder; transgenic animal; knockout animal; ss.
KW psychiatric disorder; transgenic animal; knockout animal; ss.

XX Homo sapiens.

XX	Key	Location/Qualifiers
EH		

FT	key	Education/
FT	CDS	19..1209

```

ET      /*tag= a

```

```
ET
/product="MAR1"
```

XX PN DE10021474-A1.

08-NOV-2001

03-MAY-2000: 2000DE-01021474.

03-MAY-2000: 2000DE-01021474.

XX
PA (BRIE/) BRITISH M

PA (BRUE/) BRUESS M.
PA (BOEN/) BOENISCH H.

PT Briess M. Boenisch H:

XX
DP
WPT: 2002-011956/02

DR WEI; Z00Z-011938/
DR P-PSDB: AAG80225.

PT New monoamine receptor-1 gene, MARI1, useful for diagnosis and treatment of MARI1-related diseases.

PS Disclosure: Page 4: 6pp: German.

This invention describes a novel human monoamine receptor-1 (MAR1) gene (I) which has cytostatic activity and can be used for gene therapy. (I), and derived (anti)sense oligonucleotides, are useful in treatment and diagnosis of (I)-related diseases (possibly tumours and psychiatric disorders), for producing transgenic/knockout animals, and for recombinant expression of the protein (II) that it encodes. (II) is useful in ligand-binding studies and screening assays, also for treatment and diagnosis of (II)-related diseases. This sequence encodes the human MAR1 monoamine receptor-1 protein

Sequence 1227 BP; 249 A; 383 C; 299 G; 296 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1191;		Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTCTACCATGAGTCTGTGTGGGCTATCGT	60						
Db	19	ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTCTACCATGAGTCTGTGTGGGCTATCGT	78						
QY	61	TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGTGACAGGCACCGTGGGCAATGTGCTC	120						
Db	79	TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGTGACAGGCACCGTGGGCAATGTGCTC	138						
QY	121	ACCCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGTCTATAGCC	180						
Db	139	ACCCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGTCTATAGCC	198						
QY	181	AACCTCACACTGGCTGATCTCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC	240						
Db	199	AACCTCACACTGGCTGATCTCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC	258						
QY	241	TACCTCCACCTGCACCTGGGACCCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT	300						
Db	259	TACCTCCACCTGCACCTGGGACCCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT	318						
QY	301	TTTGCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCCTCATCGCACTGGGACGCTACCTC	360						
Db	319	TTTGCCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCCTCATCGCACTGGGACGCTACCTC	378						
QY	361	CTCAATTGCCCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA	420						
Db	379	CTCAATTGCCCCACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA	438						
QY	421	CTGTFGAGCACCTGGGTTGTGGCGTGGCCAGCTTTTGCTCCCTCTTGCGCTATTATATC	480						
Db	439	CTGTFGAGCACCTGGGTTGTGGCGTGGCCAGCTTTTGCTCCCTCTTGCGCTATTATATC	498						
QY	481	CTGTFACCTGTAGTCTGCACCTGACGCTTTTGACCGCATCCGAGCCCGCCTTACACCACC	540						
Db	499	CTGTFACCTGTAGTCTGCACCTGACGCTTTTGACCGCATCCGAGCCCGCCTTACACCACC	558						
QY	541	ATCCTCATGGGCATCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC	600						
Db	559	ATCCTCATGGGCATCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC	618						
QY	601	ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCAATACAAGTTTGCACAGGCA	660						
Db	619	ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCAATACAAGTTTGCACAGGCA	678						
QY	661	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTTTCCAGGAG	720						
Db	679	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTTTCCAGGAG	738						
QY	721	CTGGACACAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT	780						
Db	739	CTGGACACAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT	798						
QY	781	GCTGCCACCAACCAGACCCCTGGAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC	840						
Db	799	GCTGCCACCAACCAGACCCCTGGAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC	858						
QY	841	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCCA	900						
Db	859	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCCA	918						
QY	901	ATTAAGGAGCCAGAAAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG	960						
Db	919	ATTAAGGAGCCAGAAAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG	978						
QY	961	TGTTTTGTGTGTTTCTCTGCTTTTGGCCTGAGCTACATCCCTTCTTGTGCTCAACATT	1020						
Db	979	TGTTTTGTGTGTTTCTCTGCTTTTGGCCTGAGCTACATCCCTTCTTGTGCTCAACATT	1038						
QY	1021	CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGTGCTGCCAACCTCACCTGG	1080						
Db	1039	CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGTGCTGCCAACCTCACCTGG	1098						

QY	1081	CTCAATGGTTGCATCAACCCCTGTGCTCTATGCAGCCATGAACCGCCAATTCCGCCAAGCA	1140
Db	1099	CTCAATGGTTGCATCAACCCCTGTGCTCTATGCAGCCATGAACCGCCAATTCCGCCAAGCA	1158
QY	1141	TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG	1191
Db	1159	TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG	1209
RESULT 3			
ACC84331			
ID	ACC84331	standard; DNA; 1311 BP.	
XX	ACC84331;		
AC	ACC84331;		
XX	03-OCT-2003	(first entry)	
DT	03-OCT-2003	(first entry)	
XX	Human hp15a	receptor coding sequence.	
DE	Human; hp15a;	receptor; G-protein coupled receptor; cardiant; gastrointestinal; gene therapy; gene; ds.	
KW	Human; hp15a;	receptor; G-protein coupled receptor; cardiant; gastrointestinal; gene therapy; gene; ds.	
KW	Human; hp15a;	receptor; G-protein coupled receptor; cardiant; gastrointestinal; gene therapy; gene; ds.	
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	CDS	61..1251	
FT		/*tag= a	
FT		/product= "hp15a"	
XX	WO2003054540-A1.		
PN	03-JUL-2003.		
XX	19-DEC-2002;	2002WO-US040612.	
PF	19-DEC-2001;	2001US-00029436.	
XX	(SYNA-)	SYNAPTIC PHARM CORP.	
PA	Smith KE,	Weinshank R;	
PI	WPI;	2003-559173/52.	
XX	P-PSDB;	ABR52422.	
DR	New recombinant nucleic acid, useful for preparing a composition for treating disorders linked to human hp15a receptor e.g. cardiovascular or gastrointestinal disorders.		
XX	Claim 1;	Fig 1A-B; 98pp; English.	
PS	The present sequence is that of nucleic acid encoding a human orphan G-protein coupled receptor, designated hp15a. The sequence was initially identified in a human placenta genomic library using probes representing transmembrane domains III, V and VI of human serotonin 5-HY1Dbeta receptor. The endogenous ligand for hp15a is likely to be a neuromodulator since the receptor is present in several regions of the human brain. The invention provides hp15a nucleic acids, vectors, host cells, antibodies, probes, antisense oligonucleotides, transgenic non-human animals, methods of isolating the receptor, methods of treating an abnormality that is associated with activity of hp15a e.g. cardiovascular or gastrointestinal disorders, and methods of determining binding of compounds to hp15a		
XX	Sequence 1311 BP;	266 A; 409 C; 315 G; 321 T; 0 U; 0 Other;	
SQ	Query Match 100.0%; Score 1191; DB 8; Length 1311; Best Local Similarity 100.0%; Pred. No. 0; Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		

QY	1	ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGGGCTATCGT	60
Db	61	ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGGGCTATCGT	120

QY	121	ACCCTACTGGCCTTGGCCATCCAGGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC	180
DB	196	ACCCTACTGGCCTTGGCCATCCAGGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC	255
QY	181	AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC	240
DB	256	AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC	315
QY	241	TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTCGGGCTCCTCCTT	300
DB	316	TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTCGGGCTCCTCCTT	375
QY	301	TTTGGCTCCAAATCTGTCTCCATCCTGACCTCTGCTGCCTCATCGCACTGGACGCTACCTC	360
DB	376	TTTGGCTCCAAATCTGTCTCCATCCTGACCTCTGCTGCCTCATCGCACTGGACGCTACCTC	435
QY	361	CTCATITGCCCAACCTAAGCTTTTTTCCCAAAGTTTTTCAGTGCCCAAGGGGATAGTCTGGCA	420
DB	436	CTCATITGCCCAACCTAAGCTTTTTTCCCAAAGTTTTTCAGTGCCCAAGGGGATAGTCTGGCA	495
QY	421	CTGGTGAGCACCTGGGTGTGGGCGTGGCCAGCTTTGCTCCTCCTCTGGCCTATTATATC	480
DB	496	CTGGTGAGCACCTGGGTGTGGGCGTGGCCAGCTTTGCTCCTCCTCTGGCCTATTATATC	555
QY	481	CTGGTACCTGTAGTGTGCACCTGCAGCTTTGACCGCATCCGAGCCGCGCTTACACCACC	540
DB	556	CTGGTACCTGTAGTGTGCACCTGCAGCTTTGACCGCATCCGAGCCGCGCTTACACCACC	615
QY	541	ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC	600
DB	616	ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC	675
QY	601	ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAGTTGGACAGGCA	660
DB	676	ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAGTTGGACAGGCA	735
QY	661	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCGTGCTTCCAGGAG	720
DB	736	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCGTGCTTCCAGGAG	795
QY	721	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCA	780
DB	796	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCA	855
QY	781	GCTGCCACCAACCCAGACCTTGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC	840
DB	856	GCTGCCACCAACCCAGACCTTGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC	915
QY	841	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCCA	900
DB	916	AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCCA	975
QY	901	ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	960
DB	976	ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	1035
QY	961	TGTTTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGCTGCTCAACATT	1020
DB	1036	TGTTTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGCTGCTCAACATT	1095
QY	1021	CTGGATGCCAGAGTCCAGGTCCTCCGGGTGGTCCATGCTTGTGCTGCCAACCTCACCTGG	1080
DB	1096	CTGGATGCCAGAGTCCAGGTCCTCCGGGTGGTCCATGCTTGTGCTGCCAACCTCACCTGG	1155
QY	1081	CTCAATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCGCCAAGCA	1140
DB	1156	CTCAATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCGCCAAGCA	1215
QY	1141	TATGGCTCCATTTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG	1191
DB	1216	TATGGCTCCATTTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG	1266

RESULT 5
AAS98070
ID AAS98070 standard; DNA; 1546 BP.
XX
XX AC AAS98070;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human DNA for potential G protein-coupled receptor #27.
XX
KW Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor;
KW Alzheimer's disease; amyotrophic lateral sclerosis; asthma;
KW atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;
KW chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
KW depression; epilepsy; macular degeneration; lymphoma; melanoma;
KW multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;
KW psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;
KW tuberculosis; cognition disorder; memory disorder; anorexia;
KW hormonal release disorder; cardiovascular activity disorder;
KW pain perception disorder; obesity; diabetes; obesity; diabetes;
KW hyperlipidaemia; stroke; gene therapy.

2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841

CC of the invention
XX SQ Sequence 1546 BP; 383 A; 442 C; 351 G; 370 T; 0 U; 0 Other;
Query Match 100.0%; Score 1191; DB 6; Length 1546;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGTATCGT 60
Db 91 ATGTGGACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGTATCGT 150
QY 61 TATGTTGACGTTAGCTGGGGGTGGTGGTGTGACAGGACCGTGGGCAATGCTC 120
Db 151 TATGTTGACGTTAGCTGGGGGTGGTGGTGTGACAGGACCGTGGGCAATGCTC 210
QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
Db 211 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 270
QY 181 AACCTCAGACTGGCTGATCTCCTCTACTGACAGCTCCCTTACGCCCCCTTCTCTGIGGACACC 240
Db 271 AACCTCAGACTGGCTGATCTCCTCTACTGACAGCTCCCTTACGCCCCCTTCTCTGIGGACACC 330
QY 241 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTCCTT 300
Db 331 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTCCTT 390
QY 301 TTGCGCTCCAAATTTCTGCTCCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTC 360
Db 391 TTGCGCTCCAAATTTCTGCTCCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTC 450
QY 361 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 420
Db 451 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 510
QY 421 CTGGTGAGACCTGGGTTGTGGGGTGGCCAGCTTTTGTCTCCCTCTGCGCTATTATATC 480
Db 511 CTGGTGAGACCTGGGTTGTGGGGTGGCCAGCTTTTGTCTCCCTCTGCGCTATTATATC 570
QY 481 CTGGTACCTGTAGTCTGACCTGACCTTTCACCGCATCCGAGCCGCGCTTACACACC 540
Db 571 CTGGTACCTGTAGTCTGACCTGACCTTTCACCGCATCCGAGCCGCGCTTACACACC 630
QY 541 ATCCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 600
Db 631 ATCCTCATGGGCATCTACTTTGTGCTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 690
QY 601 ATCCACCGCAGGTCAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 660
Db 691 ATCCACCGCAGGTCAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 750
QY 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGCTTCCAGGAG 720
Db 751 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGCTTCCAGGAG 810
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCACT 780
Db 811 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCACT 870
QY 781 GCTGCCACCCAGACCCCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 840
Db 871 GCTGCCACCCAGACCCCTGGAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 930
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 900
Db 931 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 990
QY 901 ATTAAGGAGCCAGAGAGCTCCGATTTCTTCATCGGAATTTGGGAGGTGACTCGAATG 960
Db 991 ATTAAGGAGCCAGAGAGCTCCGATTTCTTCATCGGAATTTGGGAGGTGACTCGAATG 1050
QY 961 TGTTTGTGTTCTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020

Db 1051 TGTTTGTGTTCTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1110
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCAGCTGG 1080
Db 1111 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCAGCTGG 1170
QY 1081 CTCAATGTTGTCATCAACCTGTGCTCTATGCGCCATGACCGCCCAATTCCGCCACCA 1140
Db 1171 CTCAATGTTGTCATCAACCTGTGCTCTATGCGCCATGACCGCCCAATTCCGCCACCA 1230
QY 1141 TATGGCTCCATTTTAAAAAGAGGGCCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1231 TATGGCTCCATTTTAAAAAGAGGGCCCCCGGAGTTTCCATAGGCTCCATTAG 1281
RESULT 6
ABT17029
ID ABT17029 standard; DNA; 1546 BP.
XX
AC ABT17029;
XX
DT 03-APR-2003 (first entry)
XX
DE Human MP21 gene EX33 SEQ ID No 3.
XX
KW Cytostatic; p21 pathway modulating agent; cancer; angiogenic; apoptotic;
KW cell proliferation disorder; MP21; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003006990-A1.
XX
PD 23-JAN-2003.
XX
PF 10-JUL-2002; 2002WO-US021549.
XX
PR 12-JUL-2001; 2001US-0305017P.
PR 10-OCT-2001; 2001US-0328491P.
PR 15-FEB-2002; 2002US-0357452P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Li D, Funke RP;
XX
DR WPI; 2003-221779/21.
DR P-PSDB; ABJ19755.
XX
PT Identifying candidate p21 pathway modulator, by contacting an assay
PT system having modifiers of p21 polypeptide or gene with a test agent to
PT provide a reference activity in system and detecting test agent-biased
PT activity.
XX
PS Example; Page 55-56; 199pp; English.
XX
CC The invention relates to a novel method for identifying a candidate p21
CC pathway modulating agent. The novel method comprises contacting an assay
CC system, comprising a purified MP21 polypeptide (modifier of p21) or
CC nucleic acid, with a test agent under conditions, so that but for the
CC presence of a test agent, the assay system provides a reference activity
CC and detection of test agent-biased activity of the assay system. The
CC novel method of the invention is useful for identifying a candidate p21
CC pathway modulating agent. The invention also includes a method for
CC modulating the p21 pathway of a cell, and a method for diagnosing a
CC disease e.g. cancer in a patient. The identified modulators are useful in
CC diagnosis, therapy and pharmaceutical development. The modulators are
CC useful in a variety of diagnostic and therapeutic applications including
CC angiogenic, apoptotic and cell proliferation disorders. This
CC polynucleotide sequence represents a gene encoding an MP21 protein of the
XX invention
SQ Sequence 1546 BP; 383 A; 442 C; 351 G; 370 T; 0 U; 0 Other;

Query Match				100.0%;	Score 1191;	DB 7;	Length 1546;				
Best Local Similarity				100.0%;	Pred. No. 0;						
Matches 1191;				Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
QY	1	ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTACTACCATGAGTCTGTGCTGGCTATCGT	60								
Db	91	ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTACTACCATGAGTCTGTGCTGGCTATCGT	150								
QY	61	TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGTGACAGGCACCGTGGGCAATGTGCTC	120								
Db	151	TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGTGACAGGCACCGTGGGCAATGTGCTC	210								
QY	121	ACCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC	180								
Db	211	ACCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC	270								
QY	181	AACCTCACACTGGCTGATCTCCTCTACTGCAAGCTCCTTTCAGCCCTTCTCTGTGGACACC	240								
Db	271	AACCTCACACTGGCTGATCTCCTCTACTGCAAGCTCCTTTCAGCCCTTCTCTGTGGACACC	330								
QY	241	TACCTCCACCTGCCTGGCGCACCGGTGCCACCTTCTGCAAGGTATTTGGGCTCCTCCTT	300								
Db	331	TACCTCCACCTGCCTGGCGCACCGGTGCCACCTTCTGCAAGGTATTTGGGCTCCTCCTT	390								
QY	301	TTTGCTCTCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC	360								
Db	391	TTTGCTCTCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC	450								
QY	361	CTCATTTGCCACCCCTAAGCTTTTTTCCCAAGTTTTTTCAGTGCCCAAGGGATAGTGTGGCA	420								
Db	451	CTCATTTGCCACCCCTAAGCTTTTTTCCCAAGTTTTTTCAGTGCCCAAGGGATAGTGTGGCA	510								
QY	421	CTGCTGAGCACCTGGGTTGTGGCGGTGGCCAGCTTTTGTCTCCCTCTGCGCTATTATATC	480								
Db	511	CTGCTGAGCACCTGGGTTGTGGCGGTGGCCAGCTTTTGTCTCCCTCTGCGCTATTATATC	570								
QY	481	CTGSTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGGCCGCGCTTACACCACC	540								
Db	571	CTGSTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGGCCGCGCTTACACCACC	630								
QY	541	ATCCTCATGGGCATCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC	600								
Db	631	ATCCTCATGGGCATCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC	690								
QY	601	ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACCTGGACCAATACAAAGTTGCGACAGGCA	660								
Db	691	ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACCTGGACCAATACAAAGTTGCGACAGGCA	750								
QY	661	AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTGTTCCAGGAG	720								
Db	751	AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTGTTCCAGGAG	810								
QY	721	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGTAGGGGATTTTCATCTGAGCCAGTCAGT	780								
Db	811	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGTAGGGGATTTTCATCTGAGCCAGTCAGT	870								
QY	781	GCTGCCACCCAGACCCCTGGAAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC	840								
Db	871	GCTGCCACCCAGACCCCTGGAAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC	930								
QY	841	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGGCCA	900								
Db	931	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGGCCA	990								
QY	901	ATTAAAGGAGCCAGAAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG	960								
Db	991	ATTAAAGGAGCCAGAAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG	1050								
QY	961	TGTTTTGCTGTGTTTCTCTGCTTTTGGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT	1020								
Db	1051	TGTTTTGCTGTGTTTCTCTGCTTTTGGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT	1110								
QY	1021	CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACTCACCTGG	1080								

RESULT 7

ABZ42551 standard; DNA; 1546 BP.

AC ABZ42551;

DT 04-MAR-2003 (first entry)

XX Human G protein-coupled receptor EX33 nucleotide SEQ ID NO:584.

G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
G protein-coupled receptor modulator; antibody; immune-related disease;
growth-related disease; cell regeneration-related disease; AIDS; cancer;
immunological-related cell proliferative disease; autoimmune disease;
Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
ulcer; gene; ds.

XX Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US050107.

PR 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burmer GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX P-PSDB; ABP81705.

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (i) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections,

CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 1546 BP; 383 A; 442 C; 351 G; 370 T; 0 U; 0 Other;
Query Match 100.0%; Score 1191; DB 7; Length 1546;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db |||||
QY 91 ATGTGGACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 150
Db |||||
QY 61 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 120
Db |||||
QY 151 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 210
Db |||||
QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
Db |||||
QY 211 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 270
Db |||||
QY 181 AACCTCAGACTGGCTGATCTCCTCTACTGCACGCTCCTTACGCCCTTCTCTGTGGACACC 240
Db |||||
QY 271 AACCTCAGACTGGCTGATCTCCTCTACTGCACGCTCCTTACGCCCTTCTCTGTGGACACC 330
Db |||||
QY 241 TACCTCAGCTGCACTGGCGACCGGTGCCACCTTCTGAGGGTATTGCGCTCCTCCTT 300
Db |||||
QY 331 TACCTCAGCTGCACTGGCGACCGGTGCCACCTTCTGAGGGTATTGCGCTCCTCCTT 390
Db |||||
QY 301 TTGCGCTCCAAATCTGTCTCCATGCTGACCTCTGCTGATCGGCTGAGGACGCTACCTC 360
Db |||||
QY 391 TTGCGCTCCAAATCTGTCTCCATGCTGACCTCTGCTGATCGGCTGAGGACGCTACCTC 450
Db |||||
QY 361 CTCATTGCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTCTGGCA 420
Db |||||
QY 451 CTCATTGCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTCTGGCA 510
Db |||||
QY 421 CTGGTGAGCACTGGGTTGTGGGCTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 480
Db |||||
QY 511 CTGGTGAGCACTGGGTTGTGGGCTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 570
Db |||||
QY 481 CTGGTACCTGTAGTCTGACCTGCGAGCTTTTGACCGCATCCGAGCGCGCTTACACCACC 540
Db |||||
QY 571 CTGGTACCTGTAGTCTGACCTGCGAGCTTTTGACCGCATCCGAGCGCGCTTACACCACC 630
Db |||||
QY 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTCCTC 600
Db |||||
QY 631 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTCCTC 690
Db |||||
QY 601 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 660
Db |||||
QY 691 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 750
Db |||||
QY 661 AGCATCCACTCCAACCATGTGSCCAGGACTGATGAGGSCATGCTGCTGCTTCCAGGAG 720
Db |||||
QY 751 AGCATCCACTCCAACCATGTGSCCAGGACTGATGAGGSCATGCTGCTGCTTCCAGGAG 810
Db |||||
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCACT 780
Db |||||
QY 811 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCACT 870
Db |||||
QY 781 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
Db |||||
QY 871 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 930
Db |||||

QY 841 AAGAGAGCTAAGCAGATGGCAGAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCA 900
Db |||||
QY 931 AAGAGAGCTAAGCAGATGGCAGAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCA 990
Db |||||
QY 901 ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db |||||
QY 991 ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1050
Db |||||
QY 961 TGTTTTGCTGTGTTCTCTCTGCTTTCCTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db |||||
QY 1051 TGTTTTGCTGTGTTCTCTCTGCTTTCCTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1110
Db |||||
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCACTGG 1080
Db |||||
QY 1111 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCACTGG 1170
Db |||||
QY 1081 CTCAATGTTGTCATCAACCTGTGCTCTATGAGCCATGAACGCCCAATTCCGCCAAGCA 1140
Db |||||
QY 1171 CTCAATGTTGTCATCAACCTGTGCTCTATGAGCCATGAACGCCCAATTCCGCCAAGCA 1230
Db |||||
QY 1141 TATGGTCCCATTTTAAAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db |||||
QY 1231 TATGGTCCCATTTTAAAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1281
Db |||||
RESULT 8
AAI99548
ID AAI99548 standard; cDNA; 1579 BP.
XX
AC AAI99548;
XX
DT 04-JAN-2002 (first entry)
XX
DE Human expressed polynucleotide SEQ ID NO 11.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antistickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200155387-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001310.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465573/50.

P-PSDB; AAM99936.

Isolated digestive system associated polypeptide for treating, preventing and/or prognosing disorders related to the digestive system including digestive system cancers and also for testing and detection e.g. diagnosis.

Claim 1; SEQ ID NO 11; 509pp + Sequence Listing; English.

The invention relates to novel genes (AAI99548-AAI99604) and proteins (AAM99936-AAM99984) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, diabetes mellitus, Crohn's disease, anaemia, autoimmune thyroiditis, diabetes mellitus, ulcerative colitis; (c) multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (d) wound healing cardiovascular disorders such as myocardial ischaemias; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1579 BP; 356 A; 460 C; 381 G; 379 T; 0 U; 3 Other;
Query Match 100.0%; Score 1191; DB 4; Length 1579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT 60
Db 112 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGTGGGCTATCGT 171
QY 61 TATGTTGCAAGTTAGCTGGGGGTGGTGGTGGTGTGTGACAGGCACCGTGGGCAATGTGCTC 120
Db 172 TATGTTGCAAGTTAGCTGGGGGTGGTGGTGGTGTGTGACAGGCACCGTGGGCAATGTGCTC 231
QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTC AACCTGCTCATAGCC 180
Db 232 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTC AACCTGCTCATAGCC 291
QY 181 AACCTCAGACTGGCTGATCTCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACACC 240
Db 292 AACCTCAGACTGGCTGATCTCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACACC 351
QY 241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTCCTT 300
Db 352 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTCCTT 411
QY 301 TTTGCCCTCAATTTCTGCTCCATCTGACCTGACCTCTGCTCATCGCACTGGGACGTACCTC 360
Db 412 TTTGCCCTCAATTTCTGCTCCATCTGACCTGACCTCTGCTCATCGCACTGGGACGTACCTC 471
QY 361 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATAGTGTGGCA 420
Db 472 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATAGTGTGGCA 531
QY 421 CTGGTGAGCACCTGGTGTGGGGGTGGCCAGCTTTGCTCCCTCTGGCCCTATTATATC 480
Db 532 CTGGTGAGCACCTGGTGTGGGGGTGGCCAGCTTTGCTCCCTCTGGCCCTATTATATC 591
QY 481 CTGGTACCTGTAGTCTGCACCTGCACTTTGACCGCATCCGAGGCCGCTTACACCACC 540
Db 592 CTGGTACCTGTAGTCTGCACCTGCACTTTGACCGCATCCGAGGCCGCTTACACCACC 651
QY 541 ATCCTCATGGGCATCTACTTTGCTTGGCTCAGCAGTGTGGCATCTTCTATTTGCCTC 600
Db 652 ATCCTCATGGGCATCTACTTTGCTTGGCTCAGCAGTGTGGCATCTTCTATTTGCCTC 711
QY 601 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGACCAATACAAAGTTGCGACAGGCA 660
Db 712 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGACCAATACAAAGTTGCGACAGGCA 771
QY 661 AGCATCACTCCAACTATGTGCCAGGACTGTATGAGGCCATGCTGCTGTTCCAGGAG 720
Db 772 AGCATCACTCCAACTATGTGCCAGGACTGTATGAGGCCATGCTGCTGTTCCAGGAG 831
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCACT 780
Db 832 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCACT 891
QY 781 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
Db 892 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 951
QY 841 AAGAGAGTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 900
Db 952 AAGAGAGTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 1011
QY 901 ATTAAAGGAGCCAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 1012 ATTAAAGGAGCCAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG 1071
QY 961 TGTGTTGCTGTGTTCTCTGCTTTGCTGCTGAGCTACATCCCTCTTCTGCTGCTCAACATT 1020

Db 1072 TGTGTTGCTGTGTTCTCTGCTTTGCTGCTGAGCTACATCCCTCTTCTGCTGCTCAACATT 1131
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGCTGCCAACCTCACTGG 1080
Db 1132 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGCTGCCAACCTCACTGG 1191
QY 1081 CTCAATGTTGTCATCAACCTCTGCTCTATGTCAGCCATGAACCGCAATTCGCCAAGCA 1140
Db 1192 CTCAATGTTGTCATCAACCTCTGCTCTATGTCAGCCATGAACCGCAATTCGCCAAGCA 1251
QY 1141 TATGGCTCCATTTTAAAGAGAGGCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1252 TATGGCTCCATTTTAAAGAGAGGCCCGGAGTTTCCATAGGCTCCATTAG 1302
RESULT 9
AAH78712
ID AAH78712 standard; cDNA; 1595 BP.
XX
AC AAH78712;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human EX33 G-protein coupled receptor cDNA sequence.
XX
KW G-protein coupled receptor; EX33; rheumatoid arthritis;
KW neutrophil-associated inflammatory disease; Crohn's disease;
KW ulcerative colitis; chronic obstructive pulmonary disease; COPD;
KW adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KW inflammatory bowel disease; human; GPCR; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 140..1330
FT /*tag= a
FT /product= "EX33 protein"
XX
PN WO200166597-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-EP002462.
XX
PR 06-MAR-2000; 2000US-00518832.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Jarai G, Cooper PR, Yousefi S;
XX
DR WPI; 2001-541917/60.
XX
PT Use of an inflammatory related G-protein coupled receptor (EX33), a
PT polynucleotide encoding it or other compounds (e.g. antibodies) in the
PT diagnosis or treatment of a neutrophil-associated inflammatory disease,
PT e.g. rheumatoid arthritis.
XX
PS Claim 3; Page 29; 32pp; English.
XX
CC The present nucleic acid sequence represents cDNA encoding EX33, a human
CC inflammatory disease-related G-protein coupled receptor (GPCR). G-protein
CC coupled receptors are important targets in therapeutic applications
CC because they are involved in a wide variety of physiological and
CC pathological processes. The invention comprises the use of the EX33
CC polypeptide and polynucleotide in the diagnosis or treatment of a
CC neutrophil-associated inflammatory disease. The EX33 polypeptide, EX33
CC polynucleotide, an antibody specific to the EX33 polypeptide, and an
CC antisense oligonucleotide/polynucleotide probe specific to the EX33
CC polynucleotide are useful in the diagnosis or treatment of neutrophil-
CC associated inflammatory diseases, such as chronic obstructive pulmonary
CC disease (COPD), adult respiratory distress syndrome (ARDS), rheumatoid
CC arthritis, and inflammatory bowel diseases (e.g., Crohn's disease and

CC	ulcerative colitis)
XX	
SQ	Sequence 1595 BP; 393 A; 459 C; 365 G; 378 T; 0 U; 0 Other;
	Query Match 100.0%; Score 1191; DB 4; Length 1595;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
DB	
QY	140 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 199
DB	
QY	61 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 120
DB	
QY	200 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 259
DB	
QY	121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
DB	
QY	260 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 319
DB	
QY	181 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTCAGCCCTTCTCTGTGGACACC 240
DB	
QY	320 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTCAGCCCTTCTCTGTGGACACC 379
DB	
QY	241 TACCTCCACCTGCACCTGGCGCACCCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTT 300
DB	
QY	380 TACCTCCACCTGCACCTGGCGCACCCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTT 439
DB	
QY	301 TTTGGCTCCAATTCTGTCTCCATCCTGACCCCTTGCCCTCATCGCACTGGGACGCTACCTC 360
DB	
QY	440 TTTGGCTCCAATTCTGTCTCCATCCTGACCCCTTGCCCTCATCGCACTGGGACGCTACCTC 499
DB	
QY	361 CTCATTGCCACCCCTAAGCTTTTTCGCCAAGTTTTCAGTGCCCAAGGGGATAGTCTGGCA 420
DB	
QY	500 CTCATTGCCACCCCTAAGCTTTTTCGCCAAGTTTTCAGTGCCCAAGGGGATAGTCTGGCA 559
DB	
QY	421 CTGGTGAGCACTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCCTATTTATATC 480
DB	
QY	560 CTGGTGAGCACTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCCTATTTATATC 619
DB	
QY	481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCCGATCCGAGGCCGCTTACACCACC 540
DB	
QY	620 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCCGATCCGAGGCCGCTTACACCACC 679
DB	
QY	541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTCTC 600
DB	
QY	680 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTCTC 739
DB	
QY	601 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCAATACAAGTTGCGACAGGCA 660
DB	
QY	740 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCAATACAAGTTGCGACAGGCA 799
DB	
QY	661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTTCCAGGAG 720
DB	
QY	800 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTTCCAGGAG 859
DB	
QY	721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 780
DB	
QY	860 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 919
DB	
QY	781 GCTGCCACCAACCCAGACCTTGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
DB	
QY	920 GCTGCCACCAACCCAGACCTTGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 979
DB	
QY	841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
DB	
QY	980 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 1039
DB	
QY	901 ATTAAGGAGCCGAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
DB	
QY	1040 ATTAAGGAGCCGAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG 1099
DB	
QY	961 TGTTTTGCTGTGTTCTCTGCTTTTGCCCTGAGCTACATCCCCTTCTTGCTGCTCAACATT 1020

PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236328P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-488777/53.
XX
PT New nucleic acid molecules encoding 49 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Disclosure; SEQ ID NO 130; 524pp; English.
XX
CC The present invention relates to the isolation of novel human uterine
CC motility-association polypeptides (AAU18094-AAU18152), and cDNA and
CC genomic sequences encoding for these polypeptides. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with uterine motility such as pregnancy
CC and labour, and menstrual disorders. The polynucleotide sequences of the
CC invention are also useful in gene therapy. AAS28995-AAS29020 represent
CC genomic sequences encoding for novel human uterine motility-association
CC polypeptides. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;

Query Match 100.0%; Score 1191; DB 4; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db |||||||
QY 61 TATGTTGCAGTTAGCTGGGGGTTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 120
Db |||||||
QY 697 TATGTTGCAGTTAGCTGGGGGTTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 756
QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
Db |||||||
QY 757 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
QY 181 AACCTCACACTGGTGTATCTCTCTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 240
Db |||||||
QY 817 AACCTCACACTGGTGTATCTCTCTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 876

QY 241 TACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 300
Db |||||
QY 877 TACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 936
Db |||||
QY 301 TTGCGCTCCAATTCTGTCTCCATCCTGCACCTCTGCCTCATCGCACTGGACGCTACCTC 360
Db |||||
QY 937 TTGCGCTCCAATTCTGTCTCCATCCTGCACCTCTGCCTCATCGCACTGGACGCTACCTC 996
QY 361 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTCTGGCA 420
Db |||||
QY 997 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTCTGGCA 1056
QY 421 CTGGTGAGCACCTGGGTTCTGGGCGTGGCCAGCTTGTCTCCCTCTCTGGCCCTATTATATC 480
Db |||||
QY 1057 CTGGTGAGCACCTGGGTTCTGGGCGTGGCCAGCTTGTCTCCCTCTCTGGCCCTATTATATC 1116
QY 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCCGATCCGAGGCCCGCCCTTACACCACC 540
Db |||||
QY 1117 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCCGATCCGAGGCCCGCCCTTACACCACC 1176
QY 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCGCTC 600
Db |||||
QY 1177 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCGCTC 1236
QY 601 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACTGGACCAATCAAGTTCCGACAGGCA 660
Db |||||
QY 1237 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACTGGACCAATCAAGTTCCGACAGGCA 1296
QY 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGCCCATGCCCTGGTCTGTTCCAGGAG 720
Db |||||
QY 1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGCCCATGCCCTGGTCTGTTCCAGGAG 1356
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGAGCCAGTGGGATTTTCATCTGAGCCAGTCAGT 780
Db |||||
QY 1357 CTGGACAGCAGGTTAGCATCAGGAGGAGCCAGTGGGATTTTCATCTGAGCCAGTCAGT 1416
QY 781 GGTGCCACACCCAGACCCCTGGAAAGGGGACTCATCAGAAAGTGGGAGCCAGATCAACAGC 840
Db |||||
QY 1417 GGTGCCACACCCAGACCCCTGGAAAGGGGACTCATCAGAAAGTGGGAGCCAGATCAACAGC 1476
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCA 900
Db |||||
QY 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCA 1536
QY 901 ATTAAGGAGCCAGAGGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db |||||
QY 1537 ATTAAGGAGCCAGAGGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
QY 961 TGTTTGTGCTGTTCCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1020
Db |||||
QY 1597 TGTTTGTGCTGTTCCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1656
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCATGCTTGTGCCAACCTCACCTGG 1080
Db |||||
QY 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCATGCTTGTGCCAACCTCACCTGG 1716
QY 1081 CTCATGTGTTGCATCAACCTGTGCTCTATGCGAGCCATGAACCGCAATTCCGCCAAGCA 1140
Db |||||
QY 1717 CTCATGTGTTGCATCAACCTGTGCTCTATGCGAGCCATGAACCGCAATTCCGCCAAGCA 1776
QY 1141 TATGGTCCATTATTAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db |||||
QY 1777 TATGGTCCATTATTAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1827
Db |||||

RESULT 11

AAS30237

ID AAS30237 standard; DNA; 2046 BP.

XX

AC AAS30237;

XX

DT 21-NOV-2001 (first entry)

XX DNA encoding renal and cardiovascular-associated protein, Seq ID 155.
DE Human; antiinflammatory; neuroprotective; immunomodulator; vulnery;
XX cardiovascular; cytostatic; nephrotropic; antianaemic; nephritis;
KW immunosuppressive; kidney disorder; renal failure; hypertension;
KW cardiovascular disorder; myocardial infarction; blood disorder; anaemia;
KW blood coagulation disorder; electrolyte imbalance disorder; cancer;
KW hyponatraemia; hyperkalaemia; neoplastic disorder; nephroma;
KW autoimmune disease; inflammatory disease; reproductive system disorder;
KW endocrine disorder; neural activity; neurological disorder;
KW wound healing; respiratory disorder; ss.

XX Homo sapiens.

PN WO200155328-A2.

XX 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US001359.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226686P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 08-SEP-2000; 2000US-0232081P.

PR 12-SEP-2000; 2000US-0231968P.

Db 997 CTCATTGCCCCACCCTAAGCTTTTTCCTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGCTGGCA 1056
Qy 421 CTGGTGAGCACCTGGGTTGTGGCGGTGGCCAGCTTGTCTCCCTCTGGCCCTATTATATC 480
Db 1057 CTGGTGAGCACCTGGGTTGTGGCGGTGGCCAGCTTGTCTCCCTCTGGCCCTATTATATC 1116
Qy 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGGCCGGCCCTTACACCACC 540
Db 1117 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGGCCGGCCCTTACACCACC 1176
Qy 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 600
Db 1177 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 1236
Qy 601 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGGCAGAGGCA 660
Db 1237 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGGCAGAGGCA 1296
Qy 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCCATGCCTGGTCGTTTCCAGGAG 720
Db 1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCCATGCCTGGTCGTTTCCAGGAG 1356
Qy 721 CTGGACAGCAGGTTAGCATCAGGAGGAGCCCGACTCATCAGAAGTGGGAGCCAGATCAACAGC 840
Db 1357 CTGGACAGCAGGTTAGCATCAGGAGGAGCCCGACTCATCAGAAGTGGGAGCCAGATCAACAGC 1416
Qy 781 GCTGCCACCAACCAGACCTTGAAGGGGACTCATCAGAAGTGGGAGCCAGATCAACAGC 840
Db 1417 GCTGCCACCAACCAGACCTTGAAGGGGACTCATCAGAAGTGGGAGCCAGATCAACAGC 1476
Qy 841 AAGAGAGCTAAGCAGATGCGAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
Db 1477 AAGAGAGCTAAGCAGATGCGAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 1536
Qy 901 ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 1537 ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
Qy 961 TGTGTTGCTGTGTTCCCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1020
Db 1597 TGTGTTGCTGTGTTCCCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1656
Qy 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCATGCTTGTGCTGCCAACCTCACCTGG 1080
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCATGCTTGTGCTGCCAACCTCACCTGG 1716
Qy 1081 CTCAATGGTTGCATCAACCTGTGCTCTATGAGCATGAACCGCCAAATTCGCCCAAGCA 1140
Db 1717 CTCAATGGTTGCATCAACCTGTGCTCTATGAGCATGAACCGCCAAATTCGCCCAAGCA 1776
Qy 1141 TATGGCTCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1777 TATGGCTCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1827

RESULT 12
AAS35064
ID AAS35064 standard; DNA; 2046 BP.
XX
AC AAS35064;
XX
DT 04-DEC-2001 (first entry)
XX
DE DNA #14 encoding human neoplastic disease associated polypeptide.
XX
KW Human; neoplastic disease associated polypeptide; cancer; gene therapy;
KW hyperproliferative disorder; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic; ds.
XX
OS Homo sapiens.
XX

PN WO200155163-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001358.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.

QY	601	ATCCACCGCCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAGTTTGGACAGGCA	660	07-JUL-2000; 2000US-0216647P
Db	1237	ATCCACCGCCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAGTTTGGACAGGCA	1296	07-JUL-2000; 2000US-0216880P
QY	661	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCAATGCCTGGTCGTTTCCAGGAG	720	11-JUL-2000; 2000US-0217487P
Db	1297	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCAATGCCTGGTCGTTTCCAGGAG	1356	11-JUL-2000; 2000US-0217496P
QY	721	CTGGACAGCAGGTTTAGCATCAGGAGGACCCAGTGGAGGATTTTCATCTGAGCCAGTCAGT	780	14-AUG-2000; 2000US-0218290P
Db	1357	CTGGACAGCAGGTTTAGCATCAGGAGGACCCAGTGGAGGATTTTCATCTGAGCCAGTCAGT	1416	14-AUG-2000; 2000US-0220963P
QY	781	GCTGCCACCAACCCAGACCCCTGGAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC	840	26-JUL-2000; 2000US-0220964P
Db	1417	GCTGCCACCAACCCAGACCCCTGGAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC	1476	14-AUG-2000; 2000US-0224518P
QY	841	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA	900	14-AUG-2000; 2000US-0224519P
Db	1477	AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA	1536	14-AUG-2000; 2000US-0225213P
QY	901	ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	960	14-AUG-2000; 2000US-0225214P
Db	1537	ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG	1596	14-AUG-2000; 2000US-0225266P
QY	961	TGTTTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT	1020	14-AUG-2000; 2000US-0225447P
Db	1597	TGTTTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT	1656	14-AUG-2000; 2000US-0225757P
QY	1021	CTGGATGCCAGAGTCCAGGCTCCCCGGGTGCTCCAGTGTCCATGCTTGTGCCAACCCTCACCTGG	1080	14-AUG-2000; 2000US-0225758P
Db	1657	CTGGATGCCAGAGTCCAGGCTCCCCGGGTGCTCCAGTGTCCATGCTTGTGCCAACCCTCACCTGG	1716	14-AUG-2000; 2000US-0225759P
QY	1081	CTCAATGTTGTCATCAACCCCTGTGCTCTATGCGAGCCATGAACCGCCAATTCGCGCAAGCA	1140	18-AUG-2000; 2000US-0226279P
Db	1717	CTCAATGTTGTCATCAACCCCTGTGCTCTATGCGAGCCATGAACCGCCAATTCGCGCAAGCA	1776	22-AUG-2000; 2000US-0226681P
QY	1141	TATGGCTCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG	1191	22-AUG-2000; 2000US-0226688P
Db	1777	TATGGCTCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG	1827	22-AUG-2000; 2000US-0227182P
RESULT 13				
AAK77581				
ID	AAK77581	standard; DNA; 2046 BP.		
XX	AC			
XX	XX			
DT	07-NOV-2001	(first entry)		
DE	Human	immune/haematopoietic antigen genomic sequence	SEQ ID NO:32393.	
DE	Human;	immune; haematopoietic; immune/haematopoietic antigen; cancer;		
KW	cytostatic;	gene therapy; vaccine; metastasis; ds.		
XX	Homo sapiens.			
OS	WO200157182-A2.			
PN	09-AUG-2001.			
XX	17-JAN-2001;	2001WO-US001354.		
PF	31-JAN-2000;	2000US-0179065P.		
XX	04-FEB-2000;	2000US-0180628P.		
PR	24-FEB-2000;	2000US-0184664P.		
PR	02-MAR-2000;	2000US-0186350P.		
PR	16-MAR-2000;	2000US-0189874P.		
PR	17-MAR-2000;	2000US-0190076P.		
PR	18-APR-2000;	2000US-0198123P.		
PR	19-MAY-2000;	2000US-0205515P.		
PR	07-JUN-2000;	2000US-0209467P.		
PR	28-JUN-2000;	2000US-0214886P.		
PR	30-JUN-2000;	2000US-0215135P.		

PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246603P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 32393; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)

CC polynucleotides may be used to produce the secreted (I), by inserting the
-CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX

SQ Sequence 2046 BP; 500 A; 525 C; 515 G; 506 T; 0 U; 0 Other;

Query Match 100.0%; Score 1191; DB 4; Length 2046;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
|||
Db 637 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 696
|||
QY 61 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 120
|||
Db 697 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 756
|||
QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
|||
Db 757 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
|||
QY 181 AACCTCACACTGGCTGATCTCTCTACTGACGGTCTCTTACGCCCTTCTCTGTGGACACC 240
|||
Db 817 AACCTCACACTGGCTGATCTCTCTACTGACGGTCTCTTACGCCCTTCTCTGTGGACACC 876
|||
QY 241 TACCTCCACCTGCACCTGGCCACCCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTCCTT 300
|||
Db 877 TACCTCCACCTGCACCTGGCCACCCGGTGCCACCTTCTGACGGGTATTTGGGCTCCTCCTT 936
|||
QY 301 TTTGGCTCCAAATCTGTCTCCATCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTC 360
|||
Db 937 TTTGGCTCCAAATCTGTCTCCATCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTC 996
|||
QY 361 CTCATTGCCCAACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTCTGGCA 420
|||
Db 997 CTCATTGCCCAACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTCTGGCA 1056
|||
QY 421 CTGGTGAGCACCTGGGTTGGGGCGTGGCCAGCTTTGCTCCCTCTGGCCCTATTATATC 480
|||
Db 1057 CTGGTGAGCACCTGGGTTGGGGCGTGGCCAGCTTTGCTCCCTCTGGCCCTATTATATC 1116
|||
QY 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCAGGCGGCGCTTACACCA 540
|||
Db 1117 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCAGGCGGCGCTTACACCA 1176
|||
QY 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
|||
Db 1177 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 1236
|||
QY 601 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCAATACAAAGTTGCGACAGGCA 660
|||
Db 1237 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACCTGGACCAATACAAAGTTGCGACAGGCA 1296
|||
QY 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTTCCAGGAG 720
|||
Db 1297 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTTCCAGGAG 1356
|||
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGCCAGTGGGGGATTTTCATCTGAGCCAGTCAGT 780
|||
Db 1357 CTGGACAGCAGGTTAGCATCAGGAGGCCAGTGGGGGATTTTCATCTGAGCCAGTCAGT 1416
|||
QY 781 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 840
|||
Db 1417 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 1476
|||
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 900
|||

Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCCAGCCA 1536
QY 901 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 1537 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
QY 961 TGTTTTGCTGTGTTCTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 1597 TGTTTTGCTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1656
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACCTGG 1080
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACCTGG 1716
QY 1081 CTCAATGGTTGCATCAACCCTGTGCTCTATGAGCCATGAACCGCCAAATTCGCCCAAGCA 1140
Db 1717 CTCAATGGTTGCATCAACCCTGTGCTCTATGAGCCATGAACCGCCAAATTCGCCCAAGCA 1776
QY 1141 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGTCCATTAG 1191
Db 1777 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGTCCATTAG 1827

RESULT 14
ABA06789

ID ABA06789 standard; DNA; 2046 BP.

AC ABA06789;

XX 10-JAN-2002 (first entry)

DE Human genomic DNA SEQ ID NO: 875.

XX Human; gene therapy; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; inflammation; ds.

OS Homo sapiens.

XX WO200154474-A2.

PN 02-AUG-2001..

PD 17-JAN-2001; 2001WO-US001349.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.

AC ABK44021;
XX
DT 05-JUN-2002 (first entry)
XX
DE Genomic DNA encoding novel central nervous system protein #33.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200155318-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001332.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.

121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTAACCTGCTCATAGCC 180
121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTAACCTGCTCATAGCC 180
181 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTTCAGGCTTCTCTGTGGACACC 240
181 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTTCAGGCTTCTCTGTGGACACC 240
241 TACCTCCACCTGCACTGGCGCACCGGTGCGCACCTTCTGACGGTATTGGGCTCCTCCTT 300
241 TACCTCCACCTGCACTGGCGCACCGGTGCGCACCTTCTGACGGTATTGGGCTCCTCCTT 300
301 TTTGCCCTCCAACTTCTCTCCATCCTGACCCCTCTGCTCATCGACTGGGACGCTACCTC 360
301 TTTGCCCTCCAACTTCTCTCCATCCTGACCCCTCTGCTCATCGACTGGGACGCTACCTC 360
361 CTCATTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 420
361 CTCATTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 420
421 CTGGTGAGCACCTGGGTTGTGGGCTGGCCAGCTTTTGTCTCCCTCTGGCCTATTATATC 480
421 CTGGTGAGCACCTGGGTTGTGGGCTGGCCAGCTTTTGTCTCCCTCTGGCCTATTATATC 480
481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCGGCCTTACACCACC 540
481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCGGCCTTACACCACC 540
541 ATCCTCATGGGCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCTC 600
541 ATCCTCATGGGCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCTC 600
601 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 660
601 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 660
661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGTTCCAGGAG 720
661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGTTCCAGGAG 720
721 CTGGACAGCAGGTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 780
721 CTGGACAGCAGGTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 780
781 GCTGCCACCAACCCAGACCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
781 GCTGCCACCAACCCAGACCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCTTGCCAAAGCCAGCCA 900
841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCTTGCCAAAGCCAGCCA 900
901 ATTAAGGAGCAGAGAGCTCCGGATTTCTCATCGGAATTTGGGAAGGTGACTCGAATG 960
901 ATTAAGGAGCAGAGAGCTCCGGATTTCTCATCGGAATTTGGGAAGGTGACTCGAATG 960
961 TGTTTTGTGCTTCTCTGCTTTGCTGCTAGCTACATCCCTCTTGTGCTGCTCAACATT 1020
961 TGTTTTGTGCTTCTCTGCTTTGCTGCTAGCTACATCCCTCTTGTGCTGCTCAACATT 1020
1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGCTGCCAACCTCACTGG 1080
1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGCTGCCAACCTCACTGG 1080
1081 CTCAATGGTTGCATCAACCTGTGCTTATGAGCCATGACCCGCAATTCCTCCGCAAGCA 1140
1081 CTCAATGGTTGCATCAACCTGTGCTTATGAGCCATGACCCGCAATTCCTCCGCAAGCA 1140
1141 TATGGCTCCATTTTAAAGAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
1141 TATGGCTCCATTTTAAAGAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191

RESULT 2
US-10-029-436-1
; Sequence 1, Application US/10029436
; Publication No. US20030124138A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E.
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA Encoding A Human Receptor (hpl5a) And Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 55180
; CURRENT APPLICATION NUMBER: US/10/029,436
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US/09/179,798A
; PRIOR FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-029-436-1
Query Match 100.0%; Score 1191; DB 15; Length 1311;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGTGGCTATCGT 60
Db 61 ATGTGGACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGTGGCTATCGT 120
QY 61 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 120
Db 121 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 180
QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTAACCTGCTCATAGCC 180
Db 181 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTAACCTGCTCATAGCC 240
QY 181 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTTCAGCCCTTCTCTGTGGACACC 240
Db 241 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTTCAGCCCTTCTCTGTGGACACC 300
QY 241 TACCTCCACCTGCACTGGCGCACCGGTGCGCACCTTCTGACGGTATTGGGCTCCTCCTT 300
Db 301 TACCTCCACCTGCACTGGCGCACCGGTGCGCACCTTCTGACGGTATTGGGCTCCTCCTT 360
QY 301 TTTGCCCTCCAACTTCTCTCCATCCTGACCCCTCTGCTCATCGACTGGGACGCTACCTC 360
Db 361 TTTGCCCTCCAACTTCTCTCCATCCTGACCCCTCTGCTCATCGACTGGGACGCTACCTC 420
QY 361 CTCATTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 420
Db 421 CTCATTGCCCAACCTTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 480
QY 421 CTGGTGAGCACCTGGGTTGTGGGCTGGCCAGCTTTGACCGCATCCGAGCCGGCCTTACACCACC 540
Db 481 CTGGTGAGCACCTGGGTTGTGGGCTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 540
QY 481 CTGGTACCTGTAGTCTGCACCTGCGACTTTTGACCGCATCCGAGCCGGCCTTACACCACC 600
Db 541 CTGGTACCTGTAGTCTGCACCTGCGACTTTTGACCGCATCCGAGCCGGCCTTACACCACC 600
QY 541 ATCCTCATGGGCTACTTCTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCTC 600
Db 601 ATCCTCATGGGCTACTTCTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCTC 660
QY 601 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 660
Db 661 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 720
QY 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGTTCCAGGAG 720
Db 721 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGTTCCAGGAG 780

QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTCATCTGAGCCAGTCAGT 780
Db 781 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTCATCTGAGCCAGTCAGT 840
QY 781 GCTGCCACCAACCAGACCCCTGGAAGGGAGTCTATCAGAAAGTGGAGACCAATCAACAGC 840
Db 841 GCTGCCACCAACCAGACCCCTGGAAGGGAGTCTATCAGAAAGTGGAGACCAATCAACAGC 900
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
Db 901 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 960
QY 901 ATTAAGGAGCCAGAGAGTCCCGGATTCTTCATCGGAATTGGGAAGGAGTCAATG 960
Db 961 ATTAAGGAGCCAGAGAGTCCCGGATTCTTCATCGGAATTGGGAAGGAGTCAATG 1020
QY 961 TGTTTGTGTTGTTCTCTGTTTCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 1021 TGTTTGTGTTGTTCTCTGTTTCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1080
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACCTGG 1080
Db 1081 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACCTGG 1140
QY 1081 CTCATGTTGTCATCAACCTTGCTCTATGCAGCCATGAACCGCCAATTCCGCAAGCA 1140
Db 1141 CTCATGTTGTCATCAACCTTGCTCTATGCAGCCATGAACCGCCAATTCCGCAAGCA 1200
QY 1141 TATGGCTCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1201 TATGGCTCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1251

RESULT 3

US-09-826-508-37
; Sequence 37, Application US/09826508
; Patent No. US20010025099A1
; GENERAL INFORMATION:
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Lisa Vawter
; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
; TITLE OF INVENTION: and Polynucleotides
; FILE REFERENCE: GP-70744USB
; CURRENT APPLICATION NUMBER: US/09/826,508
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 1498
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-826-508-37

Query Match 100.0%; Score 1191; DB 9; Length 1498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTGTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db 76 ATGTGGAACAGCTGTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 135
QY 61 TATGTTGCAGTTAGCTGGGGGTGGTGGCTGTGACAGGCAACGTTGGGCAATGTGCTC 120
Db 136 TATGTTGCAGTTAGCTGGGGGTGGTGGCTGTGACAGGCAACGTTGGGCAATGTGCTC 195
QY 121 ACCCTACTGGCCTGGCCATCCAGGCCAAGCTCCGTACCCGATTCACCTGCTCATAGCC 180
Db 196 ACCCTACTGGCCTGGCCATCCAGGCCAAGCTCCGTACCCGATTCACCTGCTCATAGCC 255
QY 181 AACCTCACACTGGCTGATCTCCTCTACTGCAGCTCCTTCAGCCCTTCTGTGGACACC 240
Db 256 AACCTCACACTGGCTGATCTCCTCTACTGCAGCTCCTTCAGCCCTTCTGTGGACACC 315

QY 241 TACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 300
Db 316 TACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 375
QY 301 TTTGGCTCCAAATTCGTCTCCATCCTGACCCCTCTGCCTCATCGCACCTGGACGCTACCTC 360
Db 376 TTTGGCTCCAAATTCGTCTCCATCCTGACCCCTCTGCCTCATCGCACCTGGACGCTACCTC 435
QY 361 CTCATTGCCCCACCCCTAAGCTTTTCCCCCAAGTTTTCAGTGCCAAAGGGATAGTCTGGCA 420
Db 436 CTCATTGCCCCACCCCTAAGCTTTTCCCCCAAGTTTTCAGTGCCAAAGGGATAGTCTGGCA 495
QY 421 CTGGTAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCCTATTATATC 480
Db 496 CTGGTAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGGCCCTATTATATC 555
QY 481 CTGGTAGCTGTAGTCTGCACCTGACGCTTTGACCGCATCCGAGCCCGGCTTACACCCACC 540
Db 556 CTGGTAGCTGTAGTCTGCACCTGACGCTTTGACCGCATCCGAGCCCGGCTTACACCCACC 615
QY 541 ATCCTCATGGGCATCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCTC 600
Db 616 ATCCTCATGGGCATCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCTC 675
QY 601 ATCCACCGCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 660
Db 676 ATCCACCGCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 735
QY 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 720
Db 736 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 795
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTCATCTGAGCCAGTCAGT 780
Db 796 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTCATCTGAGCCAGTCAGT 855
QY 781 GCTGCCACCAACCAGACCCCTGGAAGGGAGTCTATCAGAAAGTGGAGACCAATCAACAGC 840
Db 856 GCTGCCACCAACCAGACCCCTGGAAGGGAGTCTATCAGAAAGTGGAGACCAATCAACAGC 915
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
Db 916 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 975
QY 901 ATTAAGGAGCCAGAGAGTCCCGGATTCTTCATCGGAATTGGGAAGGAGTCAATG 960
Db 976 ATTAAGGAGCCAGAGAGTCCCGGATTCTTCATCGGAATTGGGAAGGAGTCAATG 1035
QY 961 TGTTTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 1036 TGTTTGTGTTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1095
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCACCTGG 1080
Db 1096 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCACCTGG 1155
QY 1081 CTCAATGTTGCAATCAACCCCTGTGCTCTATGAGCCCATGAACCGCCATTCGCGCAAGCA 1140
Db 1156 CTCAATGTTGCAATCAACCCCTGTGCTCTATGAGCCCATGAACCGCCATTCGCGCAAGCA 1215
QY 1141 TATGGCTCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1216 TATGGCTCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1266

RESULT 4

US-10-225-567A-584
; Sequence 584, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.

APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 584

LENGTH: 1546

TYPE: DNA

ORGANISM: Homo sapiens

US-10-225-567A-584

Query Match 100.0%; Score 1191; DB 15; Length 1546;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAACHTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db 91 ATGTGGAACAGCTCTGACGCCAACHTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 150
QY 61 TATGTTGAGTGTAGTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 120
Db 151 TATGTTGAGTGTAGTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 210
QY 121 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATCAACCTGCTCATAGCC 180
Db 211 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCCGATCAACCTGCTCATAGCC 270
QY 181 AACCTCAGACTGGCTGATCTCTCTACTGACGCTCCTTCCAGCCCTTCTCTGTGGACACC 240
Db 271 AACCTCAGACTGGCTGATCTCTCTACTGACGCTCCTTCCAGCCCTTCTCTGTGGACACC 330
QY 241 TACCTCAGCTGACTGGCGACCGGTGACCCCTTCTGAGGGTATTTGGGCTCCTCCTT 300
Db 331 TACCTCAGCTGACTGGCGACCGGTGACCCCTTCTGAGGGTATTTGGGCTCCTCCTT 390
QY 301 TTTGCTTCCAAATCTGTCTCCATCTGACCCCTCTGCTCCTCATGCGACTGGGACGCTACCTC 360
Db 391 TTTGCTTCCAAATCTGTCTCCATCTGACCCCTCTGCTCCTCATGCGACTGGGACGCTACCTC 450
QY 361 CTCAATGGCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA 420
Db 451 CTCAATGGCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA 510
QY 421 CTGGTGAGCACCTGGGTTGTGGGCTGGCCAGCTTTGCTCCCTCTGCTCCCTTATATATC 480
Db 511 CTGGTGAGCACCTGGGTTGTGGGCTGGCCAGCTTTGCTCCCTCTGCTCCCTTATATATC 570
QY 481 CTGGTGAGCTGTAGTCTGACCTGAGCTTTGACCGCATCCGAGCGGCTTACACACC 540
Db 571 CTGGTGAGCTGTAGTCTGACCTGAGCTTTGACCGCATCCGAGCGGCTTACACACC 630
QY 541 ATCCTCATGGGCACTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATGCTC 600
Db 631 ATCCTCATGGGCACTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATGCTC 690
QY 601 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGACCAATACAAAGTTGGCAGGCA 660
Db 691 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGACCAATACAAAGTTGGCAGGCA 750
QY 661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCTGCTGCTGCTTCCAGGAG 720
Db 751 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCTGCTGCTGCTTCCAGGAG 810
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCA 780
Db 811 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTTCATCTGAGCCAGTCA 870
QY 781 GCTGCCACCCAGACCCCTGGGAAGGGGACTCATCAGAAAGTGGGAGACCCAGATCAACAGC 840

Db 871 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGAGACCAGATCAACAGC 930
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
Db 931 AAGAGAGCTAAGCAGATGGCAGAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 990
QY 901 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 991 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1050
QY 961 TGTGTTGCTGTGTTCTCTGCTTTCCTGCTTTCCTGCTGAGCTACATCCCTTCTTGTCTCAACATT 1020
Db 1051 TGTGTTGCTGTGTTCTCTGCTTTCCTGCTTTCCTGCTGAGCTACATCCCTTCTTGTCTCAACATT 1110
QY 1021 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTCCAACTCACCCTGG 1080
Db 1111 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTCCAACTCACCCTGG 1170
QY 1081 CTCAATGTTGCTCATCAACCTGTGCTCTATGCGCCATGACCCCAATTCGCGCCAAAGCA 1140
Db 1171 CTCAATGTTGCTCATCAACCTGTGCTCTATGCGCCATGACCCCAATTCGCGCCAAAGCA 1230
QY 1141 TATGCTCCATTTTAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1231 TATGCTCCATTTTAAAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1281

RESULT 5

US-10-073-885-11
; Sequence 11, Application US/10073885
; Publication No. US20030096346A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0303C1
; CURRENT APPLICATION NUMBER: US/10/073,885
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1554)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-073-885-11

Query Match 100.0%; Score 1191; DB 15; Length 1579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAACHTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db 112 ATGTGGAACAGCTCTGACGCCAACHTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 171
QY 61 TATGTTGAGTGTAGTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 120
Db 172 TATGTTGAGTGTAGTGGGGGTGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 231
QY 121 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGATCCGATTCACACCTGCTCATAGCC 180
Db 232 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGATTCACACCTGCTCATAGCC 291
QY 181 AACCTCAGACTGGCTGATCTCTCTACTGACGCTCCTTCCAGCCCTTCTCTGTGGACACC 240
Db 292 AACCTCAGACTGGCTGATCTCTCTACTGACGCTCCTTCCAGCCCTTCTCTGTGGACACC 351
QY 241 TACTCCACCTGCACTGGCGACCGGTGCCACCTTCTGAGGGTATTTGGGCTCCTCCTT 300

Db 352 TACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 411
Qy 301 TTGCGCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 360
Db 412 TTGCGCTCCAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 471
Qy 361 CTCATTGCCCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTCTGGCA 420
Db 472 CTCATTGCCCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTCTGGCA 531
Qy 421 CTGGTGAGCACCTGGGTTGTGGGCGTGGCCAGCTTCTCCCTCTGGCCCTATTTATATC 480
Db 532 CTGGTGAGCACCTGGGTTGTGGGCGTGGCCAGCTTCTCCCTCTGGCCCTATTTATATC 591
Qy 481 CTGGTACCTGTAGTCTGACCTGCAGCTTTGACCGCATCCGAGGCCGCGCTTACACCACC 540
Db 592 CTGGTACCTGTAGTCTGACCTGCAGCTTTGACCGCATCCGAGGCCGCGCTTACACCACC 651
Qy 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTTGCCTC 600
Db 652 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTTGCCTC 711
Qy 601 ATCCACCGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGGACAGGCA 660
Db 712 ATCCACCGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGGACAGGCA 771
Qy 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTTCAGGAG 720
Db 772 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTTCAGGAG 831
Qy 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCAGTCAAGT 780
Db 832 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCAGTCAAGT 891
Qy 781 GCTGCCACCAACCCAGACCTTGAAGGGGACTCATCAGAAGTGGGAGCCAGATCAACAGC 840
Db 892 GCTGCCACCAACCCAGACCTTGAAGGGGACTCATCAGAAGTGGGAGCCAGATCAACAGC 951
Qy 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
Db 952 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 1011
Qy 901 ATTAAGGAGCCAGAGCTCCGGATTCTTCATCCGGAATTTGGGAAGGTGACTCGAATG 960
Db 1012 ATTAAGGAGCCAGAGCTCCGGATTCTTCATCCGGAATTTGGGAAGGTGACTCGAATG 1071
Qy 961 TGTTTGTGCTGTTCCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1020
Db 1072 TGTTTGTGCTGTTCCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTGCTCAACATT 1131
Qy 1021 CTGATGCCAGAGTCCAGGCTCCCGGGTGGTCCAGTGTCTGCTGCCAACCTCACCTGG 1080
Db 1132 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCAGTGTCTGCTGCCAACCTCACCTGG 1191
Qy 1081 CTCATGGTTGCATCAACCCCTGTGCTCTATGAGCCATGAACCGCCAATTCGGCCAAAGCA 1140
Db 1192 CTCATGGTTGCATCAACCCCTGTGCTCTATGAGCCATGAACCGCCAATTCGGCCAAAGCA 1251
Qy 1141 TATGGCTCCATTTTAAAAAGAGGSCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1252 TATGGCTCCATTTTAAAAAGAGGSCCCCGGAGTTTCCATAGGCTCCATTAG 1302

RESULT 6
US-09-798-710-1
; Sequence 1, Application US/09798710
; Publication No. US20020187947A1
; GENERAL INFORMATION:
; APPLICANT: Jarai, Gabor
; APPLICANT: Cooper, Paul Roy
; APPLICANT: Yousefi, Shida
; TITLE OF INVENTION: No. US20020187947A1e1 Gene
; FILE REFERENCE: 4-31328A/H026

; CURRENT APPLICATION NUMBER: US/09/798,710
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/XXX,XXX
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-798-710-1

Query Match 100.0%; Score 1191; DB 9; Length 1595;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db 140 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTCTACCATGAGTCTGTGCTGGGCTATCGT 199
Qy 61 TATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC 120
Db 200 TATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC 259
Qy 121 ACCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
Db 260 ACCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 319
Qy 181 AACCTCAGACTGGCTGATCTCTCTACTGCACGCTCTCTCAGCCCTTCTCTGTGGACACC 240
Db 320 AACCTCAGACTGGCTGATCTCTCTACTGCACGCTCTCTCAGCCCTTCTCTGTGGACACC 379
Qy 241 TACCTCCACCTGCACCTGGCGACCGGTGCCACCTTCTGACGGTATTTGGGCTCCTCCTT 300
Db 380 TACCTCCACCTGCACCTGGCGACCGGTGCCACCTTCTGACGGTATTTGGGCTCCTCCTT 439
Qy 301 TTTGCTCCAAATCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGATAGTCTGGCA 420
Db 440 TTTGCTCCAAATCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 499
Qy 361 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTCTGGCA 420
Db 500 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTCTGGCA 559
Qy 421 CTGGTGAGCACCTGGGTTGTGGGCGTGGCCAGCTTGTCTCCCTCTGGCCTATTTATATC 480
Db 560 CTGGTGAGCACCTGGGTTGTGGGCGTGGCCAGCTTGTCTCCCTCTGGCCTATTTATATC 619
Qy 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCGGCCTTACACCACC 540
Db 620 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCCGGCCTTACACCACC 679
Qy 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCCTC 600
Db 680 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGGCCTC 739
Qy 601 ATCCACCGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGCGACAGGCA 660
Db 740 ATCCACCGCCAGGTCAAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGCGACAGGCA 799
Qy 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTTCGTTCCAGGAG 720
Db 800 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTTCGTTCCAGGAG 859
Qy 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAAGT 780
Db 860 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGATTTTCATCTGAGCCAGTCAAGT 919
Qy 781 GCTGCCACCAACCCAGACCTTGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
Db 920 GCTGCCACCAACCCAGACCTTGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 979
Qy 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCACGCA 900

Db 980 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCGAGCCA 1039
QY 901 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 1040 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1099
QY 961 TGTCTTGTGCTGTTCTCTGCTTTGGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 1100 TGTCTTGTGCTGTTCTCTGCTTTGGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1159
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCACTGG 1080
Db 1160 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCACTGG 1219
QY 1081 CTCAATGTTGTCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCGCGCAAGCA 1140
Db 1220 CTCAATGTTGTCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCGCGCAAGCA 1279
QY 1141 TATGGCTCCATTTTAAAGAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1280 TATGGCTCCATTTTAAAGAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1330

RESULT 7

US-09-764-853-875
; Sequence 875, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 875
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-875

Query Match 100.0%; Score 1191; DB 9; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db 637 ATGTGGACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 696
QY 61 TATGTTGAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 120
Db 697 TATGTTGAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 756
QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
Db 757 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
QY 181 AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC 240
Db 817 AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC 876
QY 241 TACCTCACTGACCTGGCGACCGGTGCCACCTTCTGAGGGGTATTGGGCTCCTCCTT 300
Db 877 TACCTCACTGACCTGGCGACCGGTGCCACCTTCTGAGGGGTATTGGGCTCCTCCTT 936
QY 301 TTTGCTCCAAATCTGTCTCCATCTCCTGACCCCTCTGCTCATCGCACTGGGACGTACCTC 360
Db 937 TTTGCTCCAAATCTGTCTCCATCTCCTGACCCCTCTGCTCATCGCACTGGGACGTACCTC 996
QY 361 CTCAATGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTCTGGCA 420

Db 997 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGCGCA 1056
QY 421 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTTGTCCCTCTGGCCTATTTATATC 480
Db 1057 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTTGTCCCTCTGGCCTATTTATATC 1116
QY 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCAGGCCGGCCTTACACCACC 540
Db 1117 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCAGGCCGGCCTTACACCACC 1176
QY 541 ATCCTCATGGGCATCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
Db 1177 ATCCTCATGGGCATCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 1236
QY 601 ATCCACCCGAGGTCAACAGCAGCAGCAGCAGCTGGACCAATACAAAGTTGCGACAGCA 660
Db 1237 ATCCACCCGAGGTCAACAGCAGCAGCAGCAGCTGGACCAATACAAAGTTGCGACAGCA 1296
QY 661 AGCATCCACTCCAAACCATGTGGCAGGACTGATGAGGCCATGCTGCTGTTTCCAGGAG 720
Db 1297 AGCATCCACTCCAAACCATGTGGCAGGACTGATGAGGCCATGCTGCTGTTTCCAGGAG 1356
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGCCAGTGTGGGATTTTCATCTGAGCCAGTCACT 780
Db 1357 CTGGACAGCAGGTTAGCATCAGGAGGCCAGTGTGGGATTTTCATCTGAGCCAGTCACT 1416
QY 781 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAACTGGGAGACCAGATCAACAGC 840
Db 1417 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAACTGGGAGACCAGATCAACAGC 1476
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCA 900
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCA 1536
QY 901 ATTAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 1537 ATTAAGGAGCCAGAGAGCTCCGGATTCTTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
QY 961 TGTCTTGTGTTCTCTGCTTTCCTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 1597 TGTCTTGTGTTCTCTGCTTTCCTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1656
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACTGG 1080
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACTGG 1716
QY 1081 CTCAATGTTGTCATCAACCTGCTCTATGCAGCCATGAACCGCCAATTCGCGCAAGCA 1140
Db 1717 CTCAATGTTGTCATCAACCTGCTCTATGCAGCCATGAACCGCCAATTCGCGCAAGCA 1776
QY 1141 TATGGCTCCATTTTAAAGAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1777 TATGGCTCCATTTTAAAGAGAGGCGCCCGGAGTTTCCATAGGCTCCATTAG 1827

RESULT 8

US-09-989-442-155
; Sequence 155, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ208
; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11

;
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509

;
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,208
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,245
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17

; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14
;
Query Match 100.0%; Score 1191; DB 10; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGTATCGT 60
Db 637 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGTATCGT 696
QY 61 TATGTTGAGTTAGCTGGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120
Db 697 TATGTTGAGTTAGCTGGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 756
QY 121 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCGGATTCACCTGCTCATAGCC 180
Db 757 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCGGATTCACCTGCTCATAGCC 816
QY 181 AACCTCAGCTGCTGATCTCCTCTACTGACGCTCCCTTCCAGCCCTTCTCTGTGGACACC 240
Db 817 AACCTCAGCTGCTGATCTCCTCTACTGACGCTCCCTTCCAGCCCTTCTCTGTGGACACC 876
QY 241 TACCTCCAGCTGCTGCTGGCGCACCGGTGCCACCTTCTGAGGGTATTTGGGCTCCTCCT 300
Db 877 TACCTCCAGCTGCTGCTGGCGCACCGGTGCCACCTTCTGAGGGTATTTGGGCTCCTCCT 936
QY 301 TTTGCTCCAAATCTGTCTCCATCCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTC 360
Db 937 TTTGCTCCAAATCTGTCTCCATCCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTC 996
QY 361 CTCAATGCCCCACCTTAAGCTTTTCCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 420
Db 997 CTCAATGCCCCACCTTAAGCTTTTCCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 1056
QY 421 CTGGTGACACCTGGGTTGTGGGGTGGGCGGTGGCCAGCTTTTGTCTCCCTCTGGCCCTATTATC 480

Db 1057 CTGGTGACACCTGGGTTGTGGGGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 1116
QY 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGCGGCTTACACACC 540
Db 1117 CTGGTACCTGTAGTCTGCACCTGCAGCTTTTGACCGCATCCGAGCGGCTTACACACC 1176
QY 541 ATCCTCATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
Db 1177 ATCCTCATGGGCATCTACTTTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 1236
QY 601 ATCCACCGCCAGGTCAAACGAGCAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 660
Db 1237 ATCCACCGCCAGGTCAAACGAGCAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 1296
QY 661 AGCATCCACTCAACCATGTGSCCAGGACTGATGAGGSCATGCTGCTGTTTCCAGGAG 720
Db 1297 AGCATCCACTCAACCATGTGSCCAGGACTGATGAGGSCATGCTGCTGTTTCCAGGAG 1356
QY 721 CTGGACAGCAGTTAGCATCAGGAGGACCCAGTGAAGGATTTTCATCTGAGCCAGTCAGT 780
Db 1357 CTGGACAGCAGTTAGCATCAGGAGGACCCAGTGAAGGATTTTCATCTGAGCCAGTCAGT 1416
QY 781 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 840
Db 1417 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAGTGGGAGACCAGATCAACAGC 1476
QY 841 AAGAGACTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 900
Db 1477 AAGAGACTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 1536
QY 901 ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGTGAATG 960
Db 1537 ATTAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGTGAATG 1596
QY 961 TGTGTTGCTGTGTTCTCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 1597 TGTGTTGCTGTGTTCTCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1656
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1080
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1716
QY 1081 CTCAATGGTTCATCAACCTGCTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1140
Db 1717 CTCAATGGTTCATCAACCTGCTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1776
QY 1141 TATGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1777 TATGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1827

RESULT 9
US-764-886-84/c
; Sequence 84, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT202
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-886-84

Query Match 100.0%; Score 1191; DB 10; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db 1410 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 1351
QY 61 TATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC 120
Db 1350 TATGTTGCAGTTAGCTGGGGGGTGGTGGCTGTGACAGGCACCGTGGGCAATGTGCTC 1291
QY 121 ACCCTACTGGCCCTTGGCCCATCCAGCCCCAAGCTCCGTAACCGATTCAACCTGCTCATAGCC 180
Db 1290 ACCCTACTGGCCCTTGGCCCATCCAGCCCCAAGCTCCGTAACCGATTCAACCTGCTCATAGCC 1231
QY 181 AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCCTTTCAGCCCTTCTCTGTGGACACC 240
Db 1230 AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCCTTTCAGCCCTTCTCTGTGGACACC 1171
QY 241 TACCTCCACCTGCACCTGGCGACCGGTGGCCACCTTCTGACGGGTATTTGGGCTCCTCCTT 300
Db 1170 TACCTCCACCTGCACCTGGCGACCGGTGGCCACCTTCTGACGGGTATTTGGGCTCCTCCTT 1111
QY 301 TTTGGCTCCAAATCTGTCTCCATCCTGACCCCTCTGCCCTCATCGCACTGGGACGCTACCTC 360
Db 1110 TTTGGCTCCAAATCTGTCTCCATCCTGACCCCTCTGCCCTCATCGCACTGGGACGCTACCTC 1051
QY 361 CTCATTGCCACCCCTAAGCTTTTCCCCAAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 420
Db 1050 CTCATTGCCACCCCTAAGCTTTTCCCCAAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 991
QY 421 CTGGTGAGCACCTGGGTTGTGGSGGTGGCCAGCTTTGCTCCCTCTGCGCCTATTATATC 480
Db 990 CTGGTGAGCACCTGGGTTGTGGSGGTGGCCAGCTTTGCTCCCTCTGCGCCTATTATATC 931
QY 481 CTGGTACCTGTAGTCTGCACCTTGCAGCTTTGACCCGCATCCGAGGCCCGCCCTTACACCACC 540
Db 930 CTGGTACCTGTAGTCTGCACCTTGCAGCTTTGACCCGCATCCGAGGCCCGCCCTTACACCACC 871
QY 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTTGCCCTC 600
Db 870 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTTGCCCTC 811
QY 601 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGGCGACAGGCA 660
Db 810 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGGCGACAGGCA 751
QY 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGCTTCCAGGAG 720
Db 750 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGCTTCCAGGAG 691
QY 721 CTGGACAGAGGTTAGCATCAGGAGACCCAGTGAAGGGGATTTTCATCTGAGCCAGTCACT 780
Db 690 CTGGACAGAGGTTAGCATCAGGAGACCCAGTGAAGGGGATTTTCATCTGAGCCAGTCACT 631
QY 781 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 840
Db 630 GCTGCCACCAACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 571
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGGCCA 900
Db 570 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGGCCA 511
QY 901 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 510 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 451
QY 961 TGTTTTGTGTGTTCTCTGCTTTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 450 TGTTTTGTGTGTTCTCTGCTTTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 391
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCAGCTGG 1080
Db 390 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCAGCTGG 331

QY 1081 CTCAATGGTTGCATCAACCCCTGTGCTCTATGCAGCCATGAACCGCCAAATTCGCCCAAGCA 1140
Db 330 CTCAATGGTTGCATCAACCCCTGTGCTCTATGCAGCCATGAACCGCCAAATTCGCCCAAGCA 271
QY 1141 TATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCAYAGGCTCCATTAG 1191
Db 270 TATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCAYAGGCTCCATTAG 220
RESULT 10
US-09-764-875-1209
; Sequence 1209, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ02
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1209
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-875-1209
Query Match 100.0%; Score 1191; DB 11; Length 2046;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db 637 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTACCATGAGTCTGTGCTGGGCTATCGT 696
QY 61 TATGTTGCAGTTAGCTGGGGGTGTGCTGGCTGTGACAGGCACCGTGGGCAATGTGCTC 120
Db 697 TATGTTGCAGTTAGCTGGGGGTGTGCTGGCTGTGACAGGCACCGTGGGCAATGTGCTC 756
QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
Db 757 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
QY 181 AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGGCCCTTCTGTGGACACC 240
Db 817 AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGGCCCTTCTGTGGACACC 876
QY 241 TACCTCCACCTGCACCTGGCGCACCGGTGGCCACCTTCTGACGGGTATTTGGGCTCCTCCT 300
Db 877 TACCTCCACCTGCACCTGGCGCACCGGTGGCCACCTTCTGACGGGTATTTGGGCTCCTCCT 936
QY 301 TTTGGCTCCAAATCTGTCTCCATCCTGACCCCTCTGCCCTCATCGCACTGGGACGCTACCTC 360
Db 937 TTTGGCTCCAAATCTGTCTCCATCCTGACCCCTCTGCCCTCATCGCACTGGGACGCTACCTC 996
QY 361 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 420
Db 997 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 1056
QY 421 CTGGTGAGCACCTGGGTTGTGGGGCTGGCCAGCTTTGCTCCCTCTGGCCCTATTATATC 480
Db 1057 CTGGTGAGCACCTGGGTTGTGGGGCTGGCCAGCTTTGCTCCCTCTGGCCCTATTATATC 1116
QY 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCCGCATCCGAGGCCGCTTACACCACC 540
Db 1117 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCCGCATCCGAGGCCGCTTACACCACC 1176
QY 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
Db 1177 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 1236
QY 601 ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGGACAGGCA 660

Db 1237 ATCCACCGCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 1296
QY 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 720
Db 1297 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 1356
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCAGT 780
Db 1357 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCAGT 1416
QY 781 GCTGCCACACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGAGACCAGATCAACAGC 840
Db 1417 GCTGCCACACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGAGACCAGATCAACAGC 1476
QY 841 AAGAGAGTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGTCTGCCAAAGCCGAGCCA 900
Db 1477 AAGAGAGTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGTCTGCCAAAGCCGAGCCA 1536
QY 901 ATTAAGAGCCAGAAGAGCTCCGGATTTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 1537 ATTAAGAGCCAGAAGAGCTCCGGATTTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
QY 961 TGTCTTGTGTGTTCTCTGCTTTGCTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 1597 TGTCTTGTGTGTTCTCTGCTTTGCTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1656
QY 1021 CTGGATGCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGCTGCCAACCTCACCTGG 1080
Db 1657 CTGGATGCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGCTGCCAACCTCACCTGG 1716
QY 1081 CTCAATGTTGCATCAACCCCTGTGCTTATGCAGCCATGAACCGCCAATTCGCGCAAGCA 1140
Db 1717 CTCAATGTTGCATCAACCCCTGTGCTTATGCAGCCATGAACCGCCAATTCGCGCAAGCA 1776
QY 1141 TATGGCTCCATTTTAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1777 TATGGCTCCATTTTAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1827

RESULT 11

US-09-764-886-84/c
; Sequence 84, Application US/09764886
; Publication No. US2002008622A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT202
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-886-84

Query Match 100.0%; Score 1191; DB 13; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db 1410 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 1351
QY 61 TATGTTGAGTTAGCTGGGGGTGGTGGTGTGAGCAGGACCCGTTGGGCAATGTGCTC 120
Db 1350 TATGTTGAGTTAGCTGGGGGTGGTGGTGTGAGCAGGACCCGTTGGGCAATGTGCTC 1291
QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180

Db 1290 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 1231
QY 181 AACCTCAGACTGGCTGATCTCTTACTGACGCTCCTTACGCCCTTCTCTGTGGACACC 240
Db 1230 AACCTCAGACTGGCTGATCTCTTACTGACGCTCCTTACGCCCTTCTCTGTGGACACC 1171
QY 241 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGAGGGTATTTGGGCTCCTCCT 300
Db 1170 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGAGGGTATTTGGGCTCCTCCT 1111
QY 301 TTTGCTCCAAATTTCTCTCCATCCTGACCCCTCTGCTCATCGCACTGGGACGTACCTC 360
Db 1110 TTTGCTCCAAATTTCTCTCCATCCTGACCCCTCTGCTCATCGCACTGGGACGTACCTC 1051
QY 361 CTCAATGGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 420
Db 1050 CTCAATGGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 991
QY 421 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGCTCCCTATTTATATC 480
Db 990 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGCTCCCTATTTATATC 931
QY 481 CTGGTACTGTAGTCTGCACCTGTCAGCTTTTGACCGCATCCGAGCCGCGCTTACACGACC 540
Db 930 CTGGTACTGTAGTCTGCACCTGTCAGCTTTTGACCGCATCCGAGCCGCGCTTACACGACC 871
QY 541 ATCCTCATGGGCACTCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
Db 870 ATCCTCATGGGCACTCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 811
QY 601 ATCCACCCGCGAGGTCAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGCGACAGGCA 660
Db 810 ATCCACCCGCGAGGTCAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGCGACAGGCA 751
QY 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCACTGCTGCTGCTTCCAGGAG 720
Db 750 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCACTGCTGCTGCTTCCAGGAG 691
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCAGT 780
Db 690 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCAGT 631
QY 781 GCTGCCACACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 840
Db 630 GCTGCCACACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 571
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGTCTGCCAAAGCCGAGCCA 900
Db 570 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGTCTGCCAAAGCCGAGCCA 511
QY 901 ATTAAGAGAGCCAGAAGAGCTCCGGATTTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 510 ATTAAGAGAGCCAGAAGAGCTCCGGATTTTCATCGGAATTTGGGAAGGTGACTCGAATG 451
QY 961 TGTCTTGTGTTCTCTCTGCTTGGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 450 TGTCTTGTGTTCTCTCTGCTTGGCTGAGCTACATCCCTTCTTGTGCTCAACATT 391
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGCTGCCAACCTCACCTGG 1080
Db 390 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGCTGCCAACCTCACCTGG 331
QY 1081 CTCAATGTTGCATCAACCCCTGTGCTCTATGAGCCATGAACCGCCAATTCGCGCAAGCA 1140
Db 330 CTCAATGTTGCATCAACCCCTGTGCTCTATGAGCCATGAACCGCCAATTCGCGCAAGCA 271
QY 1141 TATGGCTCCATTTTAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 270 TATGGCTCCATTTTAAAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 220

```
; Sequence 130, Application US/09764893
; Publication No. US20020086330A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ09
; CURRENT APPLICATION NUMBER: US/09/764,893
; CURRENT FILING DATE: 2001-01-19
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-893-130

Query Match      100.0%; Score 1191; DB 13; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db      |||||||
Db      637 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 696
QY      61 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 120
Db      |||||||
Db      697 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 756
QY      121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGCTTCCATAGGCTCCATAGCC 180
Db      |||||||
Db      757 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
QY      181 AACCTCACACTGGCTGATCTCCTCTACTGCAAGCTCCCTTCCAGCCCTTCTCTGTGGACACC 240
Db      |||||||
Db      817 AACCTCACACTGGCTGATCTCCTCTACTGCAAGCTCCCTTCCAGCCCTTCTCTGTGGACACC 876
QY      241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAAGGTATTTGGGCTCCTCCTT 300
Db      |||||||
Db      877 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAAGGTATTTGGGCTCCTCCTT 936
QY      301 TTTGGCTCCAAATTTCTGTCTCCATCTGACCCCTCTGCCCTCATCGCACTGGGACGCTACCTC 360
Db      |||||||
Db      937 TTTGGCTCCAAATTTCTGTCTCCATCTGACCCCTCTGCCCTCATCGCACTGGGACGCTACCTC 996
QY      361 CTCATTGCCCCACCCCTAAGCTTTTCCCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 420
Db      |||||||
Db      997 CTCATTGCCCCACCCCTAAGCTTTTCCCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 1056
QY      421 CTGGTGAGCACCTGGGTTGTGGGGGTGGCCAGCTTTGCTCCCTCTGCGCCTATTATATC 480
Db      |||||||
Db      1057 CTGGTGAGCACCTGGGTTGTGGGGGTGGCCAGCTTTGCTCCCTCTGCGCCTATTATATC 1116
QY      481 CTGGTACCTGTAGTCTGCACCTGCAAGCTTTGACCGCATCCGAGGCCGCGCTTACACCAACC 540
Db      |||||||
Db      1117 CTGGTACCTGTAGTCTGCACCTGCAAGCTTTGACCGCATCCGAGGCCGCGCTTACACCAACC 1176
QY      541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCGCTC 600
Db      |||||||
Db      1177 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCGCTC 1236
QY      601 ATCCACCGCCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 660
Db      |||||||
Db      1237 ATCCACCGCCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCA 1296
QY      661 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGGCTGGTTCAGGAG 720
Db      |||||||
Db      1297 AGCATCCACTCCAAACCATGTGGCCAGGACTGATGAGGCCATGGCTGGTTCAGGAG 1356
QY      721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCACT 780
Db      |||||||
Db      1357 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCACT 1416
```

```
QY      781 GCTGCCACCACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 840
Db      |||||||
Db      1417 GCTGCCACCACCCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 1476
QY      841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCA 900
Db      |||||||
Db      1477 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCA 1536
QY      901 ATTAAGGAGCCAGAAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db      |||||||
Db      1537 ATTAAGGAGCCAGAAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
QY      961 TGTTTTGCTGTGTTCTCTCTGCTTTCCTTGAGCTAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db      |||||||
Db      1597 TGTTTTGCTGTGTTCTCTCTGCTTTCCTTGAGCTAGCTACATCCCTTCTTGTGCTCAACATT 1656
QY      1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGTGCTGCCAACCTCACCTGG 1080
Db      |||||||
Db      1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTGTGCTGCCAACCTCACCTGG 1716
QY      1081 CTCAATGGTTCATCAACCCCTGTGCTCTATGATGAGCCATGAACCGCCAAATTCGCGCAAGCA 1140
Db      |||||||
Db      1717 CTCAATGGTTCATCAACCCCTGTGCTCTATGATGAGCCATGAACCGCCAAATTCGCGCAAGCA 1776
QY      1141 TATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db      |||||||
Db      1777 TATGGCTCCATTTTAAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 1827
```

```
RESULT 13
US-10-073-865-130
; Sequence 130, Application US/10073865
; Publication No. US20030044904A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ09C1
; CURRENT APPLICATION NUMBER: US/10/073,865
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-073-865-130
```

```
Query Match      100.0%; Score 1191; DB 15; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db      |||||||
Db      637 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT 696
QY      61 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 120
Db      |||||||
Db      697 TATGTTGCAGTTAGCTGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGTGCTC 756
QY      121 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
Db      |||||||
Db      757 ACCCTACTGGCCTTGGCCATCCAGCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
QY      181 AACCTCACACTGGCTGATCTCCTCTACTGCAAGCTCCCTTCCAGCCCTTCTGTGGACACC 240
Db      |||||||
Db      817 AACCTCACACTGGCTGATCTCCTCTACTGCAAGCTCCCTTCCAGCCCTTCTGTGGACACC 876
QY      241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAAGGTATTTGGGCTCCTCCTT 300
Db      |||||||
Db      877 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAAGGTATTTGGGCTCCTCCTT 936
QY      301 TTTGGCTCCAAATTTCTGTCTCCATCTGCTCCATCTGACCCCTCTGCCTCATCGCACTGGGACGCTACCTC 360
```


Db 937 TTTGGCTCCAAATTTCTCTCCATCCCTGACCTCTGCCTCATCGCACTGGGACGTACCTC 996
QY 361 CTCATTGCCACCCCTAAAGCTTTTCCCAAGTTTTCAGTGCCAGGGGATAGTGTGGCA 420
Db 997 CTCATTGCCACCCCTAAAGCTTTTCCCAAGTTTTCAGTGCCAGGGGATAGTGTGGCA 1056
QY 421 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTTGTCTCCCTCTGGCCTATTTATATC 480
Db 1057 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTTGTCTCCCTCTGGCCTATTTATATC 1116
QY 481 CTGGTACCTGATCTACTTTGTCTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
Db 1177 ATCCTCATGGGCATCTACTTTGTCTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 1236
QY 601 ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 660
Db 1237 ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 1296
QY 661 AGCATCCACTCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 720
Db 1297 AGCATCCACTCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 1356
QY 721 CTGGACAGCAGGTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 780
Db 1357 CTGGACAGCAGGTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 1416
QY 781 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
Db 1417 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 1476
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGGATCTGCCAAAGCCAGCCCA 900
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGGATCTGCCAAAGCCAGCCCA 1536
QY 901 ATTAAGGAGCCAGAGACTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 1537 ATTAAGGAGCCAGAGACTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596
QY 961 TGTGTTGCTGTCTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 1597 TGTGTTGCTGTCTCTCTGCTTTGCCCTGAGCTACATCCCTTCTTGTGCTCAACATT 1656
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCAGCTGG 1080
Db 1657 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCCAACCTCAGCTGG 1716
QY 1081 CTCAATGTTGTCATCAACCCCTGTGCTCTATGAGCCATGAACCGCCAATTCGCGCAAGCA 1140
Db 1717 CTCAATGTTGTCATCAACCCCTGTGCTCTATGAGCCATGAACCGCCAATTCGCGCAAGCA 1776
QY 1141 TATGGTCCATTTTAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1777 TATGGTCCATTTTAAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTAG 1827

RESULT 14

US-10-103-313-592

; Sequence 592, Application US/10103313
; Publication No. US20030082758A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PJ207C1

; CURRENT APPLICATION NUMBER: US/10/103,313

; CURRENT FILING DATE: 2002-03-12

; NUMBER OF SEQ ID NOS: 653

; Prior Application removed - See File Wrapper or Palm

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 592
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-313-592

Query Match 100.0%; Score 1191; DB 15; Length 2046;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 60
Db 637 ATGTGGAACAGCTCTGACGCCAACTTCTCTCTGCTACCATGAGTCTGTGCTGGCTATCGT 696
QY 61 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 120
Db 697 TATGTTGCAGTTAGCTGGGGGTGGTGGTGTGACAGGACCGTGGGCAATGTGCTC 756
QY 121 ACCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180
Db 757 ACCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 816
QY 181 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 240
Db 817 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTACGCCCTTCTCTGTGGACACC 876
QY 241 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGCAAGGTATTTGGGCTCCTCCTT 300
Db 877 TACCTCCACTGCACTGGCGCACCGGTGCCACCTTCTGCAAGGTATTTGGGCTCCTCCTT 936
QY 301 TTTGCCTCCAATTTCTGTCTCCATCCTGACCCCTCTGCCCTAFGCGCACTGGGACGTACCTC 360
Db 937 TTTGCCTCCAATTTCTGTCTCCATCCTGACCCCTCTGCCCTAFGCGCACTGGGACGTACCTC 996
QY 361 CTCATTGCCACCCCTAAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATAGTGTGGCA 420
Db 997 CTCATTGCCACCCCTAAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGATAGTGTGGCA 1056
QY 421 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTTGTCTCCCTCTGGCCTATTTATATC 480
Db 1057 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTTGTCTCCCTCTGGCCTATTTATATC 1116
QY 481 CTGGTACCTGTAGTCTGCACCTGCGAGCTTTTGACCGCATCCGAGGCGGCTTACACACC 540
Db 1117 CTGGTACCTGTAGTCTGCACCTGCGAGCTTTTGACCGCATCCGAGGCGGCTTACACACC 1176
QY 541 ATCCTCATGGGCATCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
Db 1177 ATCCTCATGGGCATCTACTTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 1236
QY 601 ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 660
Db 1237 ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 1296
QY 661 AGCATCCACTCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 720
Db 1297 AGCATCCACTCAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTCTGTTCCAGGAG 1356
QY 721 CTGGACAGCAGGTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 780
Db 1357 CTGGACAGCAGGTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 1416
QY 781 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 840
Db 1417 GCTGCCACCCAGACCCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC 1476
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGGATCTGCCAAAGCCAGCCCA 900
Db 1477 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAGGATCTGCCAAAGCCAGCCCA 1536
QY 901 ATTAAGGAGCCAGAGACTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 1537 ATTAAGGAGCCAGAGACTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 1596

```
QY 961 TGTTTGCTGTGTTCCCTGCTTTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 1597 TGTTTGCTGTGTTCCCTGCTTTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1656

QY 1021 CTGATGCCAGAGTCCAGGTCCTCCCGGGTGTCACATGCTTGCTGCCAACCTCACCTGG 1080
Db 1657 CTGATGCCAGAGTCCAGGTCCTCCCGGGTGTCACATGCTTGCTGCCAACCTCACCTGG 1716

QY 1081 CTCATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCCGCCAAGCA 1140
Db 1717 CTCATGGTTGCATCAACCTGTGCTCTATGCAGCCATGAACCGCCAATTCCGCCAAGCA 1776

QY 1141 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1777 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1827

RESULT 15
US-10-094-417-3
; Sequence 3, Application US/10094417
; Publication No. US20030045685A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030045685A1el Receptors
; FILE REFERENCE: 018781-008110US
; CURRENT APPLICATION NUMBER: US/10/094,417
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/802,803
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/276,649
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR35
; NAME/KEY: CDS
; LOCATION: (1)..(1188)
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR35
US-10-094-417-3
Query Match 99.7%; Score 1188; DB 15; Length 1188;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAATTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60
Db 1 ATGTGGAACAGCTCTGACGCCAATTCTCTGCTACCATGAGTCTGTGCTGGGCTATCGT 60

QY 61 TATGTTGCAGTTAGCTGGGGGTGGTGGCTGTGACAGGACCCGTGGGCAATGTGCTC 120
Db 61 TATGTTGCAGTTAGCTGGGGGTGGTGGCTGTGACAGGACCCGTGGGCAATGTGCTC 120

QY 121 ACCCTACTGSCCTTGGCCATCCAGCCCAAGCTCCGTACCCGANTCAACCTGCTCATAGCC 180
Db 121 ACCCTACTGSCCTTGGCCATCCAGCCCAAGCTCCGTACCCGANTCAACCTGCTCATAGCC 180

QY 181 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTCAGCCCTTCTCTGIGGACACC 240
Db 181 AACCTCACACTGGCTGATCTCCTCTACTGACAGCTCCTTCAGCCCTTCTCTGIGGACACC 240

QY 241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 300
Db 241 TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTT 300
```

```
QY 301 TTTGCCCTCCAAATTTCTGTCTCCATCTCTGACCCCTCTGCCTCATGCGACTGGGACGCTACCTC 360
Db 301 TTTGCCCTCCAAATTTCTGTCTCCATCTCTGACCCCTCTGCCTCATGCGACTGGGACGCTACCTC 360

QY 361 CTCATTGCCCCACCCCTAAGCTTTTCCCCCAAGTTTTCAGTGCCAAAGGGGATAGTGCTGGCA 420
Db 361 CTCATTGCCCCACCCCTAAGCTTTTCCCCCAAGTTTTCAGTGCCAAAGGGGATAGTGCTGGCA 420

QY 421 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTTGGCCTATTATATC 480
Db 421 CTGGTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTTGGCCTATTATATC 480

QY 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGCCTTACACCACC 540
Db 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGCCTTACACCACC 540

QY 541 ATCCTCATGGGTCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 600
Db 541 ATCCTCATGGGTCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCCTC 600

QY 601 ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAATTCGACAGGCA 660
Db 601 ATCCACCGCCAGGTCAAAACGAGCAGCAGGCACTGGACCAATACAAATTCGACAGGCA 660

QY 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTTCCAGGAG 720
Db 661 AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTTCCAGGAG 720

QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 780
Db 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGATTTTCATCTGAGCCAGTCAGT 780

QY 781 GCTGCCACCAACCCAGACCCCTTGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 840
Db 781 GCTGCCACCAACCCAGACCCCTTGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGC 840

QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCCAGCCA 900
Db 841 AAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAGCCCAGCCA 900

QY 901 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 901 ATTAAGGAGCCAGAGAGCTCCGGATTTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960

QY 961 TGTTTTGCTGTGTTCTCTGCTTTGCTGAGCTACATCCCCCTTCTTGTGCTCAACATT 1020
Db 961 TGTTTTGCTGTGTTCTCTGCTTTGCTGAGCTACATCCCCCTTCTTGTGCTCAACATT 1020

QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1080
Db 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1080

QY 1081 CTCATATGGTTGCATCAACCCCTGTGCTCTATGCAGCCATGAACCGCAATTCGCGCAAGCA 1140
Db 1081 CTCATATGGTTGCATCAACCCCTGTGCTCTATGCAGCCATGAACCGCAATTCGCGCAAGCA 1140

QY 1141 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT 1188
Db 1141 TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT 1188
```

Search completed: September 24, 2004, 08:34:15
Job time : 961.703 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 22:14:09 ; Search time 3457.33 Seconds
(without alignments)
10287.096 Million cell updates/sec

Title: US-10-029-436-1_COPY_61_1251
Perfect score: 1191
Sequence: 1 atgtggaacagctctgacgc.....gttccataggctccattag 1191

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :			
EST:*			
1:	em_estba:*		
2:	em_esthum:*		
3:	em_estin:*		
4:	em_estmu:*		
5:	em_estov:*		
6:	em_estpl:*		
7:	em_estro:*		
8:	em_htc:*		
9:	gb_est1:*		
10:	gb_est2:*		
11:	gb_htc:*		
12:	gb_est3:*		
13:	gb_est4:*		
14:	gb_est5:*		
15:	em_estfun:*		
16:	em_estom:*		
17:	em_gss_hum:*		
18:	em_gss_inv:*		
19:	em_gss_pln:*		
20:	em_gss_vrt:*		
21:	em_gss_fun:*		
22:	em_gss_mam:*		
23:	em_gss_mus:*		
24:	em_gss_pro:*		
25:	em_gss_rod:*		
26:	em_gss_phg:*		
27:	em_gss_vrl:*		
28:	gb_gss1:*		
29:	gb_gss2:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	1191	100.0	1191	29	AY404787 Hmo sapi
2	1116.2	93.7	1187	29	AY404788 Pan trogl
3	889.2	74.7	1191	29	AY404789 Mus muscu
4	798.6	67.1	997	13	BX348812 BX348812

C	5	542	45.5	809	14	CD367121	UI-H-FT2-
C	6	532	44.7	903	13	BX330186	BX330186
C	7	481	40.4	721	14	CD365430	UI-H-FT2-
C	8	470	39.5	736	14	CD366881	UI-H-FT2-
	9	460.6	38.7	1201	13	BX336527	BX336527
	10	438	36.8	496	13	BX097926	BX097926
C	11	436	36.6	700	14	CD365279	UI-H-FT2-
	12	435	36.5	621	14	CD470995	LeukoS5_3
	13	420	35.3	660	12	EM726245	UI-E-EJ0-
	14	419	35.2	542	12	BM254098	515432 MA
	15	416.2	34.9	660	10	BF667988	602122233
	16	405.6	34.1	553	12	BM258181	522891 MA
	17	405	34.0	829	10	BE958211	601644675
C	18	397.6	33.4	726	14	CF739045	UI-M-HD0-
	19	392	32.9	499	12	BI773943	465705 MA
C	20	387	32.5	650	14	CD366344	UI-H-FT1-
	21	386	32.4	474	12	BM105642	509140 MA
	22	382	32.1	532	14	CD536450	LeukoN6_7
	23	364.2	30.6	498	14	CB221964	1IL22B6-B
C	24	354	29.7	588	12	BM680856	UI-E-EJ0-
	25	354	29.7	807	10	BF167811	601774636
	26	344.8	29.0	475	10	BF654980	279349 MA
	27	342.6	28.8	458	14	CD464412	CD464412
	28	334.8	28.1	572	13	EX511990	BX511990
	29	321	27.0	635	14	CD470023	LeukoS4_1
C	30	313.8	26.3	533	10	BE502961	h281G02.X
C	31	312	26.2	526	12	BG232061	naf32b01.
	32	303.2	25.5	588	14	CD465714	LeukoN1_7
	33	300.2	25.2	588	14	CD470028	LeukoS4_1
	34	299.8	25.2	572	14	CD470901	LeukoS5_3
	35	299.8	25.2	585	14	CD464304	LeukoN4_3
	36	299.2	25.1	368	10	BF706009	280136 MA
C	37	299	25.1	518	9	AI392922	tg10g11.x
	38	298.2	25.0	584	14	CD536362	LeukoN6_7
	39	293.2	24.6	587	14	CD464888	LeukoN4_5
	40	284.6	23.9	551	14	CD464476	LeukoN4_4
	41	280.6	23.6	497	10	AW213499	um56b11.y
C	42	256.4	21.5	528	12	BG235994	EG235994 naf20f04.
C	43	248.6	20.9	265	10	BF899665	IL5-MT020
	44	229.8	19.3	853	29	CNS03P70	AL254277 Tetraodon
	45	229.4	19.3	393	13	BY164857	BY164857

ALIGNMENTS

RESULT 1	AY404787	AY404787	1191 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	Homo sapiens GPR84 gene, VIRTUAL TRANSCRIPT, partial sequence,					
DEFINITION	Homo sapiens GPR84 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.					
ACCESSION	AY404787					
VERSION	AY404787.1	GI:39760764				
KEYWORDS	GSS.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 1191)					
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios					
JOURNAL	Science 302 (5652), 1960-1963 (2003)					
PUBMED	14671302					
REFERENCE	2 (bases 1 to 1191)					
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
TITLE	Direct Submission					

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1..1191
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1..>1191
/gene="GPR84"
/locus_tag="HCM2007"
ORIGIN
Query Match 100.0%; Score 1191; DB 29; Length 1191;
Best Local Similarity 100.0%; Pred. No. 3.3e-293;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGACAGCTCTGACGCCAACTCTCCTGCTACCATGATGCTGTGCTGGGCTATCGT 60
Db 1 ATGTGGACAGCTCTGACGCCAACTCTCCTGCTACCATGATGCTGTGCTGGGCTATCGT 60
QY 61 TATGTTGACATTAGCTGGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120
Db 61 TATGTTGACATTAGCTGGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120
QY 121 ACCCTACTGGCCTGGCCATCCAGCCCAAGCTCCGTACCCGATTAACCTGCTCATAGCC 180
Db 121 ACCCTACTGGCCTGGCCATCCAGCCCAAGCTCCGTACCCGATTAACCTGCTCATAGCC 180
QY 181 AACCTCAGACTGGCTGATCTCCTCTACTGACGCTCCTTACGCCCCTTCTCTGTGGACACC 240
Db 181 AACCTCAGACTGGCTGATCTCCTCTACTGACGCTCCTTACGCCCCTTCTCTGTGGACACC 240
QY 241 TACCTCCACCTGCACTGGCGCACCGGTGCGACCTTCTGACGGGTATTTGGGCTCCTCCTT 300
Db 241 TACCTCCACCTGCACTGGCGCACCGGTGCGACCTTCTGACGGGTATTTGGGCTCCTCCTT 300
QY 301 TTGGCTCCAAATCTGTCTCCATCTGACCCCTCTGCTCATCGCCTGCGGACGCTACCTC 360
Db 301 TTGGCTCCAAATCTGTCTCCATCTGACCCCTCTGCTCATCGCCTGCGGACGCTACCTC 360
QY 361 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCACCAAGGGATAGTGTGGCA 420
Db 361 CTCATTGCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCACCAAGGGATAGTGTGGCA 420
QY 421 CTGGTGACACCTGGGTTGGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 480
Db 421 CTGGTGACACCTGGGTTGGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTATATC 480
QY 481 CTGGTACCTGTAGTCTGCACCTTCAGCTTTTGACCGCATCCGAGCGCGGCTTACACCACC 540
Db 481 CTGGTACCTGTAGTCTGCACCTTCAGCTTTTGACCGCATCCGAGCGCGGCTTACACCACC 540
QY 541 ATCCTCATGGGCATCTACTTTGCTTGGGCTCAGCATGTTGGCATCTTCTATTGGCCTC 600
Db 541 ATCCTCATGGGCATCTACTTTGCTTGGGCTCAGCATGTTGGCATCTTCTATTGGCCTC 600
QY 601 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAGTTGGCAGGCA 660
Db 601 ATCCACCGCCAGGTCAAACGAGCAGCAGGCACTGGACCAATACAAGTTGGCAGGCA 660
QY 661 AGCATCCACTCCAACTATGTGCCAGGACTGTATGAGCCCATGCTGCTGCTTCCAGGAG 720
Db 661 AGCATCCACTCCAACTATGTGCCAGGACTGTATGAGCCCATGCTGCTGCTTCCAGGAG 720
QY 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTCTATGAGCCAGTCACT 780
Db 721 CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGGGGGATTTCTATCTGAGCCAGTCACT 780
QY 781 GCTGCCACCAACCCAGACCTGGAAAGGGGACTCATCAGAAAGTGGGAGACCATCAACAGC 840
Db 781 GCTGCCACCAACCCAGACCTGGAAAGGGGACTCATCAGAAAGTGGGAGACCATCAACAGC 840

QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
Db 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCCA 900
QY 901 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
Db 901 ATTAAAGGAGCCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960
QY 961 TGTGTTGCTGTTCTCTCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 TGTGTTGCTGTTCTCTCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 CTCAATGTTGCTCATCAACCCCTGTGCTCTATGAGCCATGACCCCAATTCGCGCCAGCA 1140
Db 1081 CTCAATGTTGCTCATCAACCCCTGTGCTCTATGAGCCATGACCCCAATTCGCGCCAGCA 1140
QY 1141 TATGGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db 1141 TATGGCTCCATTTTAAAGAGAGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
RESULT 2
AY404788 1187 bp DNA linear GSS 16-DEC-2003
LOCUS Pan troglodytes GPR84 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY404788
VERSION AY404788.1 GI:39760765
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 1187)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1187)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
source 1..1187
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene <1..>1187
/gene="GPR84"
/locus_tag="HCM2007"
ORIGIN
Query Match 93.7%; Score 1116.2; DB 29; Length 1187;
Best Local Similarity 94.4%; Pred. No. 4.4e-274;
Matches 1121; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 1 ATGTGGACAGCTCTGACGCCAACTCTCCTGCTACCATGATGCTGTGCTGGGCTATCGT 60

Db 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTACCATGAGTCTGTGTGGGCTATCGT 60

Qy 61 TATGTTGCAGTTAGCTGGGGGTTGGTGGCTGTGACAGGCACCCGTGGCAATGTGCTC 120

Db 61 TATGTTGCAGTTAGCTGGGGGTTGGTGGCTGTGACAGGCACCCGTGGCAATGTGCTC 120

Qy 121 ACCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180

Db 121 ACCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180

Qy 181 AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC 240

Db 181 AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC 240

Qy 241 TACCTCCACCTGCACCTGGCGCACCCGGTGCACCTTCCTGTCAGGGTATTTGGGTCCTCCTT 300

Db 241 TACCTCCACCTGCACCTGGCGCACCCGGTGCACCTTCCTGTCAGGGTATTTGGGTCCTCCTT 300

Qy 301 TTTGGCTCCAATTCTGTCTCCATCCTGACCCCTCTGCTCATCGCCTGACCTGGACGCTACCTC 360

Db 301 TTTGGCTCCAATTCTGTCTCCATCCTGACCCCTCTGCTCATCGCCTGACCTGGACGCTACCTC 360

Qy 361 CTCATTGCCCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA 420

Db 361 CTCATTGCCCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGTGGCA 420

Qy 421 CTGCTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 480

Db 421 CTGCTGAGCACCTGGGTTGTGGCGTGGCCAGCTTTGCTCCCTCTGCGCTATTATATC 480

Qy 481 CTGCTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGGCTTACACCACC 540

Db 481 CTGCTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGGCTTACACCACC 540

Qy 541 ATCCTCATGGGCATCTACTTTGTGCTTGGCCTCAGCAGTGTGGCATCTTCTATTGCTC 600

Db 541 ATCCTCATGGGCATCTACTTTGTGCTTGGCCTCAGCAGTGTGGCATCTTCTATTGCTC 600

Qy 601 ATCCACCGCCAGGTCAAACGAGCAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 660

Db 601 ATCCACCGCCAGGTCAAACGAGCAGCAGCAGGCACTGGACCAATACAAGTTGCGACAGGCA 660

Qy 661 AGCATCCACTCCAAACCATGTGGCCGGGACTGATGAGGCGCATGCTGCTGTTTCCAGGAG 720

Db 661 AGCATCCACTCCAAACCATGTGGCCGGGACTGATGAGGCGCATGCTGCTGTTTCCAGGAG 720

Qy 721 CTGGACAGCAGGTTAGCATACGAGGACCCAGTGAGGGGATTTCATCTGAGCCAGTCAGT 780

Db 721 NTGGACAGCAGGTTAGCATACGAGGACCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780

Qy 781 GCTGCCACACCCAGACCCTGGAAAGGGACTCATCAGAAAGTGGAGACCAGATCAACAGC 840

Db 781 NNNNNNACACCCAGACNNTGGAAAGGNNNNNNNTCAGAAAGTGGAGACCAGATCAACAGC 840

Qy 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCATCTGCCAAAGCCAGCCA 900

Db 841 AAGAGAGNNAAGCAGATGGCAGAGAAAGCCCTCCAGAAAGCCTCCAGAAAGCCAGCCA 900

Qy 901 ATTAAGGAGCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960

Db 901 ATTAAGGAGCAGAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATG 960

Qy 961 TGTGTTGCTGTCTCCTCTGCTTTGCTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020

Db 961 TGTGTTGCTGTCTCCTCTGCTTTGCTGCTGAGCTACATCCCTTCTTGTGCTCAACATT 1020

Qy 1021 CTGGATGCCAGACTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTCAACCTCACCTGG 1080

Db 1021 CTGGATGCCAGACTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCTCAACCTCACCTGG 1080

Qy 1081 CTCAATGGTTGATCAACCCCTGTCTATGAGCCATGAACCGGCAATTCGGCCAAAGCA 1140

Db 1081 CTCAACGGTTGATCAACCCCTGTCTATGAGCCATGAACCGGCAATTCGGCCAAAGCA 1140

Qy 1141 TATGGCTCCATTTTAAAGAGGGCCCCGGAGTTTCCATAGGCTCCA 1187

Db 1141 TATGGCTCCGTTTAAAGAGGGCCCCGGAGTTTCCGTAAGGCTCCA 1187

RESULT 3

AY404789 1191 bp DNA linear GSS 16-DEC-2003

LOCUS Mus musculus GPR84 gene, VIRTUAL TRANSCRIPT, partial sequence,

DEFINITION genomic survey sequence.

ACCESSION AY404789

VERSION AY404789.1 GI:39760766

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1191)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1191)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source

1..1191

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

gene

<1..>1191

/gene="GPR84"

/locus_tag="HCM2007"

ORIGIN

Query Match 74.7%; Score 889.2; DB 29; Length 1191;

Best Local Similarity 84.2%; Pred.No. 5.1e-216;

Matches 1002; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

Qy 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGTACCATGAGTCTGTGTGGGCTATCGT 60

Db 1 ATGTGGAACAGCTCAGATGCCAACTTCTCCTGTACCATGAGTCTGTGTGGGCTATCGA 60

Qy 61 TATGTTGCAGTTAGCTGGGGGTTGGTGGCTGTGACAGGCACCCGTGGCAATGTGCTC 120

Db 61 TACTTTGCAGTTATCTGCGGCGTGGCAGTGGCTGTGACAGGCACCGTGGCAATGTGCTC 120

Qy 121 ACCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC 180

Db 121 ACTCTGTGGCCTTGGCCATTCGTCCCAAGCTCCGAAACCCGCTTCAACCTGCTCATAGCC 180

Qy 181 AACCTCACACTGGCTGATCTCCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACACC 240

Db 181 AACCTCACCTGGCTGATCTACTCTACTGACGCTCCTGTCAGCCCTTCTCTCGTGGACACA 240

Qy 241 TACCTCCACCTGCACCTGGCGCACCCGGTGCACCTTCTGTCAGGGTATTTGGGTCCTCCTT 300

Db 241 TACCTCCACCTCCATTGGCGTACCGGCGGGTCTTCTGTAGAATATTGGAATCTCTCCTC 300

Qy 301 TTTGCTCCCAATTCTGTCTCCATCCTGACCCCTCTGCTCATCGCCTGACCTGGACGCTACCTC 360

Db 301 TTTACTTCCAAATCTGTCTCCATCCTCACCCTCTGTCTCATTTGCTTAGGACGCTACCTC 360
QY 361 CTCATTGCCCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 420
Db 361 CTCATTGCCCCACCTAAGCTTTTCCCAAGTTTTCAGTGCCAAAGGGGATAGTGTGGCA 420
QY 421 CTGGTGAGCACCTGGGTTGTGGCGTGGCGAGCTTTGCTCCCTCTGGCCTATTTATATC 480
Db 421 CTGGTGAGCACCTGGGTTGTGGCGTGGCGAGCTTTGCTCCCTCTGGCCTATTTATATC 480
QY 481 CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGCTTACACCA 540
Db 481 TTGGTGCCAGTGTCTGCACCTGCAGCTTTGACCGCATCCGAGCGCGCTTACACCA 540
QY 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
Db 541 ATCCTCATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATCTTCTATTGCTC 600
QY 601 ATCCACCGCCAGGTCAAAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGCA 660
Db 601 ATCCACCGCCAGGTCAAGCGTGCAGCTCGAGCACTGGACCAATACAAAGTTGCGACAGCA 660
QY 661 AGCATCCACTCAACCATGTGGCCAGGACTGATGAGGCCATGCTGCTGTTTCCAGGAG 720
Db 661 AGCATCCGCTCTCATAGGTGGCTGGGACACAAAGACCTGCTGCTGCTGCTGCTGCTG 720
QY 721 CTGGACAGCAGGTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCAGT 780
Db 721 CTAGACAGGGGGTTCCTCAAGAGGGCCCGAGCGAGGGGATTTTCATCTGAGCCAGTCAGT 780
QY 781 GCTGCCACCCAGCCAGACCTTGAAGGGGACTCATCAGAGTGGGAGACCAAGTCAACAGC 840
Db 781 GCTGCCACCCAGCAGACCTTGAAGGGTATTCGTCAAGAGCTGGGGCCAGGGCATTAGA 840
QY 841 AAGAGAGCTAAGCAGATGGCAGAGAAAGCCCTCCAGAGCATCTGCCAAAGCCAGCCCA 900
Db 841 AAGGAGCTCAACAGATCGCAGAGAGAGCCCTTCCAGAGTGCATCGCAAGCCCGGAA 900
QY 901 ATTAAGGAGCCAGAGAGCTCCGATTTCTCATCGGAATTTGGGAAGTGCATCGAATG 960
Db 901 ACTGCAGAGCTCGCAGAGCCACAGATGCCCATCAGAGTTCGGGAAGTGCATCGAATG 960
QY 961 TGTTTGTGTGTTCTCTCTGCTTCCCTCAGCTACATCCCTTCTTGTGCTCAACATT 1020
Db 961 TGCTTCGAGTGTCTCTCTGCTTCCCTCAGCTACATCCCTTCTTGTGCTCAACATT 1020
QY 1021 CTGGATGCCAGAGTCCAGGCTCCCGGGTGGTCCACATGCTTGTGCCAACCTCACCTGG 1080
Db 1021 CTGGACCCAGGGCCGTGCTCCAGAGTAGTGACATGGTGGTGGTGGTGGTGGTGGTGG 1080
QY 1081 CTCATGGTTGCATCAACCTGTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1140
Db 1081 CTCACAGCTGCATCAACCTGTGCTCTATGAGCCATGAACCGCAATTCGCGCAAGCA 1140
QY 1141 TATGGTCCATTTTAAAGAGGGCCCGGAGTTTCCATAGGCTCCATTA 1190
Db 1141 TATGGTCCATCTCTGAACCGGGCCACAGAGTTTCCGCGGTTCCATTA 1190

RESULT 4
BX348812 997 bp mRNA linear EST 05-MAY-2003
LOCUS BX348812 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI029YE18 5-PRIME, mRNA sequence.
ACCESSION BX348812
VERSION BX348812.1 GI:30379347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 997)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6847.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAG028ZC10_CS02667_1&cluster=6847.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAG028ZC10_CS02667_1.
FEATURES
Location/Qualifiers
1..997
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI029YE18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 67.1%; Score 798.6; DB 13; Length 997;
Best Local Similarity 98.7%; Pred. No. 6.9e-193;
Matches 823; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
QY 192 GGCTGATCTCCTCTACTGACGCTCTTTCAGCCCTTCTGTGTGGACACCTACCTCCACCT 251
Db 15 GGCTGATCTCCTCTACTGACGCTCTTTCAGCCCTTCTGTGTGGACACCTACCTCCACCT 74
QY 252 GCATGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTTTTGGCTCCAA 311
Db 75 GCATGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGCTCCTCCTTTTGGCTCCAA 134
QY 312 TTCTGTCTCCATCCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTCCTCATTTGCCCA 371
Db 135 TTCTGTCTCCATCCTGACCCCTCTGCTCATCGCACTGGGACGCTACCTCCTCATTTGCCCA 194
QY 372 CCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCACTGGTGAGCAC 431
Db 195 CCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCACTGGTGAGCAC 254
QY 432 CTGGTTGTGGCGTGGCCAGCTTGTCTCCCTCTGGCTATTTATATCCTGTGACCTGT 491
Db 255 CTGGTTGTGGCGTGGCCAGCTTGTCTCCCTCTGGCTATTTATATCCTGTGACCTGT 314
QY 492 AGTCTGCACCTGCAGCTTTGACCGCATCCGAGGCGCGCTTACACCACTCATCTCATGGG 551
Db 315 AGTCTGCACCTGCAGCTTTGACCGCATCCGAGGCGCGCTTACACCACTCATCTCATGGG 374
QY 552 CATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATTTCTATTGCCCTCATCCACCGCCA 611
Db 375 CATCTACTTTGTGCTTGGGCTCAGCAGTGTGGCATTTCTATTGCCCTCATCCACCGCCA 434
QY 612 GGTCAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCAAGCATCCACTC 671
Db 435 GGTCAACGAGCAGCAGCAGGCACTGGACCAATACAAAGTTGCGACAGGCAAGCATCCACTC 494
QY 672 CAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTGGTTCCTCCAGGAGCTGGACAGCAG 731
Db 495 CAACCATGTGGCCAGGACTGATGAGGCCATGCTGGTGGTTCCTCCAGGAGCTGGACAGCAG 554
QY 732 GTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCACTGCTGCCACCAC 791
Db 555 GTTAGCATCAGGAGGACCCAGTGAAGGGATTTTCATCTGAGCCAGTCACTGCTGCCACCAC 614
QY 792 CCAGACCTTGAAGGGGACTCATCAGAAAGTGGGAGCAGATCAACAGCAAGAGAGCTAA 851

```

|||||
Db 615 CCAGACCTGGAAGNGACTCATCAGAAAGTGGGAGACCAGATCAACAGCAAGAGAGCTAA 674
|||||
Qy 852 GCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAAGCCAGCCCAATTAAAGGAGC 911
|||||
Db 675 GCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAAG-CCAGCCCAATTAAAGGAGC 733
|||||
Qy 912 CAGAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGTGACTCGAATGTGTTTGTCTGT 971
|||||
Db 734 CAGAAGAGCTNCGNATTTCTCATCGGGATTGGGGAGGTGACTCGAATGTGTNTGCTGN 793
|||||
Qy 972 GTTCCTCTGCTTTGCCCTGAGCTACATCCCC-TTCTTGCTGCTCAACATTTCTGG 1024
|||||
Db 794 GTTCCTCTGCTTTGCCCTGAGCTACATCCCCTTTCTTGCTGCTTAACATTTCTG 847

RESULT 5
CD367121/c
LOCUS
DEFINITION
  UI-H-FT2-bjp-1-20-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
  UI-H-FT2-bjp-1-20-0-UI 3', mRNA sequence.
ACCESSION
  CD367121
VERSION
  CD367121.1 GI:31151211
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 809)
AUTHORS
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Dr. Gary W. Hunninghake, U of I
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/cgap.html
  Seq primer: M13 FORWARD
  POLYA=Yes.

FEATURES
      Location/Qualifiers
          1..809
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="UI-H-FT2-bjp-1-20-0-UI"
              /tissue_type="Aveolar Macrophage"
              /dev_stage="Adult"
              /lab_host="NCI CGAP FT2"
              /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP FT2 is a subtraced cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
subtracted according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. The tissue was provided by Dr.
Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 45.5%; Score 542; DB 14; Length 809;
Best Local Similarity 99.1%; Pred. No. 2.6e-127;
Matches 575; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

Qy 612 GGTCAACGAGCAGCACAGGCACTGGACCAATAACAAGTTGGCAGAGCGCAAGCATCCACTC 671
|||||
Db 809 GGTCAACGAGCAGCACAGGCACTGGACC-ATACAAGTTGGCAGAGCGCAAGCATCCACTC 751
|||||
```

```

672 CAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCTTTCCAGGAGCTGGACAGCAG 731
|||||
Db 750 CANCCATGTGGCCAGGACTGATGAGNCCATGCCTGGTCTTTCCAGGAGCTGGACAGCAG 691
|||||
Qy 732 GTTAGCATCAGGAGGACCCAGTCCAGTGGGGATTTCATCTGAGCAGTCTGCTGCCACCAC 791
|||||
Db 690 GTTAGCATCAGGAGGACCCAGTCCAGTGGGGGA-TTCATCTGAGCAGTCTGAGTGTG- 633
|||||
Qy 792 CCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGCAAGAGAGCTAA 851
|||||
Db 632 CCAGACCCCTGGAAGGGGACTCATCAGAAAGTGGGAGACCAGATCAACAGCAAGAGAGCTAA 573
|||||
Qy 852 GCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAAGCCAGCCCAATTAAAGGAGC 911
|||||
Db 572 GCAGATGGCAGAGAAAAGCCCTCCAGAAAGCATCTGCCAAAAGCCAGCCCAATTAAAGGAGC 513
|||||
Qy 912 CAGAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATGTGTTTGTCTGT 971
|||||
Db 512 CAGAAGAGCTCCGGATTCTTCATCGGAATTTGGGAAGGTGACTCGAATGTGTTTGTCTGT 453
|||||
Qy 972 GTTCCTCTGCTTTGCCCTGAGCTACATCCCCCTTCTTGCTGCTCAACATTTCTGGATGCCAG 1031
|||||
Db 452 GTTCCTCTGCTTTGCCCTGAGCTACATCCCCCTTCTTGCTGCTCAACATTTCTGGATGCCAG 393
|||||
Qy 1032 AGTCCAGGCTCCCCGGGTGGTCCATGCTTGCTGCCAACCTCACCTGGCTCAATGGTTG 1091
|||||
Db 392 AGTCCAGGCTCCCCGGGTGGTCCATGCTTGCTGCCAACCTCACCTGGCTCAATGGTTG 333
|||||
Qy 1092 CATCAACCCCTGTGCTCTATGCAGCCATGAACCGCCAAATTCGCCAAGCATATGGCTCCAT 1151
|||||
Db 332 CATCAACCCCTGTGCTCTATGCAGCCATGAACCGCCAAATTCGCCAAGCATATGGCTCCAT 273
|||||
Qy 1152 TTTAAAAAGAGGGGCCCCGGAGTTTCCATAGGCTCCATTAG 1191
|||||
Db 272 TTTAAAAAGAGGGGCCCCGGAGTTTCCATAGGCTCCATTAG 233
|||||

RESULT 6
BX330186/c
LOCUS
DEFINITION
  BX330186 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
  clone CS0DI029YE18 3-PRIME, mRNA sequence.
ACCESSION
  BX330186
VERSION
  BX330186.1 GI:30307910
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 903)
AUTHORS
  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
  Full-length cDNA libraries and normalization
JOURNAL
  Unpublished (2001)
COMMENT
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 6847.r For
  more information about this cluster, see
  http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAK055DE01NM
  1&cluster=6847.r. Contact : Feng Liang Email : fliang@lifetech.com
  URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0BAK055DE01NM1.
      Location/Qualifiers
          1..903
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="CS0DI029YE18"
              /tissue_type="PLACENTA COT 25-NORMALIZED"
              /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

FEATURES
      source
```


ACCESSION CD366881
VERSION CD366881.1 GI:31150971
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 736)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
1..736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjp-k-21-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI-CGAP FT2"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI-CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCGG"

FEATURES
source

ORIGIN

Query Match 39.5%; Score 470; DB 14; Length 736;
Best Local Similarity 99.2%; Pred. No. 6.4e-109;
Matches 503; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 685 AGGACTGATGAGGCCATGCCTGGTTCCTCCAGGAGCTGGACAGCAGGTTAGCATCAGGA 744
Db |||||
QY 736 AGGACTGATGAGNCCATGCCTGGTTCCTCCAGGAGCTGGACAGCAGGTTAGCATCAGGA 677
Db |||||
QY 745 GGACCCAGTGAGGGGATTTCATCTGAGCCAGTCAGTGTGCGCACCCAGCCAGCCCTGGAA 804
Db |||||
QY 676 GGACCCAGTGA-GGGATTTTCATCTGAGCCAGTCAGTGTGCGCACCCAGCCCTGGAA 618
Db |||||
QY 805 GGGGACTCATCAGAAGTGGGAGACCAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAG 864
Db |||||
QY 617 -GGGACTCATCAGAAGT-GGAGACCAGATCAACAGCAAGAGAGCTAAGCAGATGGCAGAG 560
Db |||||
QY 865 AAAAGCCCTCCAGAAGCATCTGCCAAAGCCCAGCCCAATTAAGGAGCCAGAGAGCTCCG 924
Db |||||
QY 559 AAAAGCCCTCCAGAAGCATCTGCCAAAGCCCAGCCCAATTAAGGAGCCAGAGAGCTCCG 500
Db |||||
QY 925 GATTCCTCATCGGAATTTGGGAAGGTGACTCGAATGTGTTTGTCTGTGTTTCTCTGCTTT 984
Db |||||
QY 499 GATTCCTCATCGGAATTTGGGAAGGTGACTCGAATGTGTTTGTCTGTGTTTCTCTGCTTT 440
Db |||||
QY 985 GCCCTGAGTACATCCCCTTCTTGTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCC 1044
Db |||||
QY 439 GCCCTGAGTACATCCCCTTCTTGTGCTCAACATTTCTGGATGCCAGAGTCCAGGCTCCC 380
Db |||||

QY 1045 CGGGTGTCCACATGCTTGTGCAACCTCACCTGGTCAATGGTTGCATCAACCCCTGTG 1104
Db |||||
QY 379 CGGGTGTCCACATGCTTGTGCAACCTCACCTGGTCAATGGTTGCATCAACCCCTGTG 320
Db |||||
QY 1105 CTCTATGCAGCCATGAACCGCAATTCGCCAAGCATATGGTCCATTAAAAAGAGGG 1164
Db |||||
QY 319 CTCTATGCAGCCATGAACCGCAATTCGCCAAGCATATGGTCCATTAAAAAGAGGG 260
Db |||||
QY 1165 CCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db |||||
QY 259 CCCCGGAGTTTCCATAGGCTCCATTAG 233
Db |||||

RESULT 9

QY 1165 CCCCGGAGTTTCCATAGGCTCCATTAG 1191
Db |||||

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

Db 285 GCCAACCTCAGACTGTGTCTGATCTCACTTAATGACGGCTCTCTTCTAGCCCTTTTC 344
QY 230 CTGTGGACACTACCTCCAC-----CTGCACCTGGCGCACCGG---TGCCACCTTCTGCAG 281
Db 345 ATGTGGACACTCTACTCTCMACTCTTGTCACTGGCGCACCTGTTGCTTACCTTCTGCAG 404
QY 282 GGTATTGGGCTCTCTCTTTTGGCTCCCAATTCTGTCTC----CATCCTGACCCCTCTGCC 337
Db 405 GGTATTGGGCTCTCTCTTTTGGCTCCCAATTCTGTCTC----CATCCTGACCCCTCTGCC 464
QY 338 TCATCGCACTGGGACGCTACCTCTCACTGCTCCACCCCTTAAGCTTTTCCCAAGTTTTC 397
Db 465 AMATMGMAATGGGAMGATAATCTTAATGTCAMAMCTAAGATTTTMMCAAGTTTTC 524
QY 398 GTGCCAAGGGGATAGTCTGGCACTGGTGAGCACCTGGGTTGTGGCGGTGGCCAGCTTTG 457
Db 525 GTGCCAAGGGKATAGTCTGGCACTGGTGAGMACCTKGGTTGTGGCGGTGGCCAGCTTTG 584
QY 458 CTCCCTCTGGCCCTATTATATCTCTGTACCTGTAGTCTGCACCTGCAGCTTTGACC-GC 516
Db 585 MTCCCTCTGGCCCTATTATATCTCTGTACCTGTAGTCTGCACCTGCAGCTTTGACCAGC 644
QY 517 ATCCGAGGCGGCGCTTACACCCACCTCAT-GGGCATCTACTTTGTGCTTGGGCTCAG 575
Db 645 ATCCGAGGCGGCGCTTACACCCACCTCATAGGKYATYACTTTGTGCTTTGGGCTCAS 704
QY 576 CAGTGTGGCATCTTCTATTGGCTCATCCACCGCCAGGTCAACAGGACGACGACGCACT 635
Db 705 CAKTTTGGKATCTTCTATTTCCTCATCCACCGCCAGGTCAACAGGACGACGCACT 764
QY 636 GGACCAATACAAAGTTGGACAGGCGAAGCATCCACTCCACCATGTGGCCAGGACTGATGA 695
Db 765 GGACCAATACAAAGTTGGACAGGCGAAGCATCCACTCCAAACATKTTGGCCAKGACTGATGA 824
QY 696 GGCCATGCTGCTGCTTTCCAGGAGCTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGA 755
Db 825 GGCATK--CYTKKTCGTTCCAGGAGCTGKACA-CAGGTTAGCATCAGGAGGACCATGTA 881
QY 756 GGGGATTTCATCTGAGCCAGTCACTGCTGCCACCAAGGAGGAGGAGGAGGAGTATC 815
Db 882 GGGGA-TTCATCTKAGCGAGTCAKTGK---CSACGACGAGACCTGGAAGKAGTATC 936
QY 816 AGAAGTGGGAGACCAAGATCAACAGCAAGAGAGC 848
Db 937 AGARTGGKTTWCAATAAMARWATAGAGCTAGC 969

RESULT 10
BX097926 496 bp mRNA linear EST 04-FEB-2003
LOCUS BX097926 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGp998P215199 ;
DEFINITION IMAGE:2108420, mRNA sequence.
ACCESSION BX097926
VERSION BX097926.1 GI:27829067
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 - (bases 1 to 496)
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998P215199.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.

FEATURES
source
1..496
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998P215199 ; IMAGE:2108420"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/clone_lib="NCI CGAP CLL1"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATTTGTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 36.8%; Score 438; DB 13; Length 496;
Best Local Similarity 100.0%; Pred. No. 7.8e-101; Mismatches 0; Indels 0; Gaps 0;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCAATGAGTCTGTGCTGGCTATCGT 60
Db 59 ATGTGGAACAGCTCTGACGCCAACTTCTCTGCTACCAATGAGTCTGTGCTGGCTATCGT 118
QY 61 TATGTTGCAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGCTC 120
Db 119 TATGTTGCAGTTAGCTGGGGGGTGGTGGTGGTGTGACAGGCACCGTGGGCAATGCTC 178
QY 121 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCGATTCAACCTGCTCATAGCC 180
Db 179 ACCCTACTGGCTTGGCCATCCAGCCCAAGCTCCGTACCGATTCAACCTGCTCATAGCC 238
QY 181 AACCTGACACTGGCTGATCTCTCTACTGACGCTCCCTCAGCCCTTCTCTGTGGACACC 240
Db 239 AACCTGACACTGGCTGATCTCTCTACTGACGCTCCCTCAGCCCTTCTCTGTGGACACC 298
QY 241 TACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGAGGGTATTTGGGCTCCTCCTT 300
Db 299 TACCTCCACCTGCACCTGGCGCACCGGTGCCACCTTCTGAGGGTATTTGGGCTCCTCCTT 358
QY 301 TTTGCTCCCAATTCTGTCTCCATCTGACCCCTCTGCTCCATCGCACTGGGACGCTACCTC 360
Db 359 TTTGCTCCCAATTCTGTCTCCATCTGACCCCTCTGCTCCATCGCACTGGGACGCTACCTC 418
QY 361 CTCATTGCCCCACCTTAAGCTTTTCCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 420
Db 419 CTCATTGCCCCACCTTAAGCTTTTCCCCAAGTTTTCAGTGCCCAAGGGATAGTGTGGCA 478
QY 421 CTGTGAGCACCTGGGTT 438
Db 479 CTGTGAGCACCTGGGTT 496

RESULT 11
CD365279/c
LOCUS CD365279 700 bp mRNA linear EST 29-MAY-2003
DEFINITION UI-H-FT2-bjj-k-21-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
UI-H-FT2-bjj-k-21-0-UI 3', mRNA sequence.
ACCESSION CD365279
VERSION CD365279.1 GI:31149369
KEYWORDS EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 700)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Gary W. Hunninghake, U of I cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html Seq primer: M13 FORWARD POLYA=Yes.

FEATURES source

```

Location/Qualifiers
1..700
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjj-k-21-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP FT2 is a substracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
subtracted according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. The tissue was provided by Dr.
Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SFO=GCCCATGCCG"

```

ORIGIN

```
Query Match      .      36.6%; Score 436; DB 14; Length 700;
Best Local Similarity 98.9%; Pred. No. 3.1e-100;
Matches 469; Conservative 0; Mismatches 2; Indels 3; Gaps 3;
```

	718	GAGCTGGACAGCAGGTTAGCATCAGGAGGCCCCAGTGAGGGGATTTCATCTGAGCCAGT	777
Qy			
D _b	700	GAGCTGGACAGCAGGTTAGCATCAGGAGGCCCCAGTGAGGGGA-NTTCATCTGAGCCAGT	642

[illegible]

QY 838 AGCAAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATGTGCCAAAGCCCG 897

Dp 583 AGCAAGAGAGCTAAGCAGATGGCAGAGAAAAGCCCTCCAGAAGCATGTGCCAAAGCCCG 524

QY	898	CCAA	TTAA	AGG	ACC	AGA	AGCT	CCGG	ATTCTT	CATCG	GAATT	TGGGA	AGGTG	ACTCGA	957
pb	523	CCAA	TTAA	AGG	ACC	AGA	AGCT	CCGG	ATTCTT	CATCG	GAATT	TGGGA	AGGTG	ACTCGA	464

QY 958 ATGTGTTTTGCTGTGTTCTCTCTGCTTTGCCCTGAGCTACATCCCCTTCTTGTGCTGCTCAAC 1017
|||||
Dh 453 ATCTGTTTTTGGCTGCTGCTGCTGCTTTGCCCTGAGCTACATCCCCTTCTTGTGCTGCTCAAC 1004
|||||

[illegible][illegible][illegible]

JOURNAL
COMMENT

Contact: Cordonnier-Pratt MM⁻
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; tissue and RNA were prepared in the Department of Large
Animal Medicine, University of Georgia; sequencing done in the
Laboratory for Genomics and Bioinformatics, University of Georgia.
Sequence ends have been trimmed to exclude vector and regions below
phred quality 16. Three-prime sequences are presented as their
reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAGGTGCG).

FEATURES

1. 621

/organism="Equus caballus"
/mol_type="mRNA"
/strain="Dartmoor Pony"
/db_xref="taxon:9796"
/clone="LeukoS5_3_D04_A027"
/sex="male"
/tissue_type="blood"
/cell_type="leukocytes"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Stimulated peripheral blood leukocytes S5"
/note="Organ: Circulatory system; Vector: pME18S-FL3;
Site_1: XhoI; Site_2: XhoI; The library was prepared from
polyA+ RNA from equine peripheral blood leukocytes
isolated from a healthy adult horse. The leukocytes were
stimulated for 4 hr with 10 ng/ml E. coli Q55:B5 LPS.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGTGTG, 3-prime DraIII site is
CACCATTGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 36.5%; Score 435; DB 14; Length 621;
Best Local Similarity 91.1%; Pred. No. 5.2e-100;
Matches 462; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 ATGTGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGTATCGT 60
|||
Db 115 ATGTGGAACAACTCTGATGCCAACTTCTCCTGCTACCAAGAGTCTGTGCTAGGCTATCGT 174

61 TATGTTGCAGTTAGCTGGGGGTGGTGGCTGTGACAGCACCGTGGGCAATGTGCTC 120

QY 179 CCAACCTCAGACTGGCTGATCTCCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACA 238
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
282 CCAACCTCAGACTGGCTGATCTCCTCTACTGACGCTCCTTCAGCCCTTCTCTGTGGACA 341
QY 239 CCTACCTCCACCTGCACTGGCGGACCGGTGCCACCTTCTGCAGGGT-ATTTGGGCTCCTC 297
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
342 CCTACCTCCACCTGCACTGGCGGACCGGTGCCACCTTCTGCAGGGTGATTTGGGCTCCTC 401
QY 298 CTTTTTGGCTCCAAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTAC 357
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
402 CTTTTTGGCTCCAAATTCTGTCTCCATCCTGACCCCTCTGCCTCATCGCACTGGGACGCTAC 461
QY 358 CTCCTCATTTGCCCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGCTG 417
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
462 CTCCTCATTTGCCCCACCCCTAAGCTTTTCCCAAGTTTTCAGTGCCCAAGGGGATAGTGCTG 521
QY 418 G-CACCTGGTGAGCACCTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCTCTGGCCTATTTA 476
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
522 GCCACTGGTGAGCACCTGGGTTGTGGGCGTGGCAGCTTTGTCCCCCTCT---GGCTATTTA 578
QY 477 TATCCTGGTACCTGTAGTCTGCACCTGCAGCTT 509
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
579 TATCCTGGTA-CTGTAGTCTGCACCTGGGGTTT 610

Search completed: September 24, 2004, 04:48:26
Job time : 3459.33 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 04:48:37 ; Search time 133 Seconds
(without alignments)
841.269 Million cell updates/sec

Title: US-10-029-436-2
Perfect score: 2041
Sequence: 1 MNWSSDANFSCYHESVLGYR.....PRQAYGSILKGRPSFRLH 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2041	100.0	396	2	AAW62598 Human 7-t
2	2041	100.0	396	4	AAG77798 Human EX3
3	2041	100.0	396	5	AAG80225 Human MAR
4	2041	100.0	396	5	ABP95618 Human GPC
5	2041	100.0	396	6	ABJ19755 Human MP2
6	2041	100.0	396	6	ABP81705 Human G p
7	2041	100.0	396	6	ABB82500 Human TGR
8	2041	100.0	396	6	ABR62422 Human hp1
9	2041	100.0	404	4	AAM99936 Human exp
10	1748	85.6	396	6	ABB82509 Mouse TGR
11	570	27.9	115	4	AAM87595 Human imm
12	568	27.8	124	5	ABB89377 Human pol
13	454	22.2	116	4	AAU18097 Human pol
14	454	22.2	116	4	AAU18646 Renal and
15	454	22.2	116	4	AAU21583 Novel hum
16	454	22.2	116	4	AAM99963 Human exp
17	454	22.2	116	4	ABB10174 Human cdn
18	454	22.2	116	4	AAU87123 Novel cen
19	454	22.2	116	4	AAU18292 Human end
20	454	22.2	116	5	ABJ05724 Novel hum
21	454	22.2	116	5	ABP66761 Human pol
22	454	22.2	116	6	ABU97261 Human pol
23	454	22.2	116	7	ADC46224 Human neo
24	378	18.5	634	4	ABB60554 Drosophil
25	373	18.3	633	7	AAE38154 Fruit fly

26	338	16.6	386	4	ABB59683	Drosophil
27	338	16.6	386	4	AAU38928	Drosophil
28	338	16.6	386	7	ADC35766	Drosophil
29	338	16.6	392	4	AAU09940	Drosophil
30	309	15.1	572	4	ABB60541	Drosophil
31	293.5	14.4	414	2	AAU11800	Human ret
32	293.5	14.4	414	6	ABU62490	Human pit
33	290.5	14.2	515	2	AAU59668	Hamster a
34	290	14.2	443	2	AAU05541	Human pit
35	290	14.2	443	2	AAU11497	Human dopa
36	290	14.2	443	2	AAU01600	Human pit
37	290	14.2	443	4	AAU76292	Human D2
38	290	14.2	443	4	AAU69075	Human dop
39	290	14.2	443	5	AAU51019	Human D2
40	290	14.2	443	6	ADA83796	Human DRD
41	290	14.2	443	6	ABP81809	Human dop
42	290	14.2	443	6	ABG73545	Human pit
43	290	14.2	443	6	ABU62489	Human pit
44	290	14.2	445	7	ADC86205	Human GPC
45	288.5	14.1	497	5	ABB04302	Hamster w

ALIGNMENTS

RESULT 1
AAW62598
ID AAW62598 standard; protein; 396 AA.
XX
AC AAW62598;
XX
DT 07-OCT-1998 (first entry)
XX
DE Human 7-transmembrane receptor, HNFJD15.
XX
KW G-protein coupled receptor; HNFJD15; treatment; diagnosis; infection;
KW HIV-1; HIV-2; cancer; screening; human; 7-transmembrane receptor;
KW Parkinson's disease; vaccine.
XX
OS Homo sapiens.
XX
PN EP853125-A2.
XX
PD 15-JUL-1998.
XX
PF 20-NOV-1997; 97EP-00309347.
XX
PR 09-JAN-1997; 97US-00775428.
XX
(SMIK) SMITHKLINE BEECHAM CORP.
XX
Sathé-GM, Fuetterer WS, Bergsma DJ, Ellis C;
XX
WPI; 1998-364650/32.
XX
N-PSDB; AAV38513.
XX
Human G-protein coupled receptor, HNFJD15 - used e.g. in treatment and
diagnosis of infections e.g. by HIV-1, HIV-2 and cancers and screening of
antagonistic or agonistic compounds.
XX
Claim 15; Fig 1; 19pp; English.
XX
This represents a human 7-transmembrane receptor, HNFJD15. HNFJD15 is a
human G-protein coupled receptor and can be used in vaccines to protect
mammals from infections e.g. bacterial, fungal, protozoan and viral
infections (especially infections caused by HIV-1 or HIV-2), cancers and
Parkinson's disease. The HNFJD15 polypeptides can be used to produce
antibodies which are used to treat such infections, isolate or identify
clones expressing the polypeptide or to purify the polypeptide. The
polypeptides can also be used to screen for compounds binding to,
activating or inhibiting activation of HNFJD15. They can be used to
diagnose diseases and susceptibility to diseases related to expression or
activity of HNFJD15

XX Sequence 396 AA;
SQ
Query Match 100.0%; Score 2041; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 1e-200;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNWSSDANFSCYHESVLGYRYVAVSWGVAVTGTVGNVLTLLALAIQPKLRTRENLIA 60
Db 1 MNWSSDANFSCYHESVLGYRYVAVSWGVAVTGTVGNVLTLLALAIQPKLRTRENLIA 60
QY 61 NLTADLLYCTLLQPFSSVDTYLHLHWTGATFCRVFGLLFASNSVSILTCLIALGRL 120
Db 61 NLTADLLYCTLLQPFSSVDTYLHLHWTGATFCRVFGLLFASNSVSILTCLIALGRL 120
QY 121 LIAHPKLPQVFSKAGIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSKAGIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQALDQYKLRQASIHNSHVARTDEAMPGRFQE 240
Db 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQALDQYKLRQASIHNSHVARTDEAMPGRFQE 240
QY 241 LDSRLASGGPSEGISSEPVSAATTQTLGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 300
Db 241 LDSRLASGGPSEGISSEPVSAATTQTLGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 300
QY 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNLTLDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNLTLDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVYAAMNRQFRQAYGSIKRGPRSFHRLH 396
Db 361 LNCINPVLVYAAMNRQFRQAYGSIKRGPRSFHRLH 396

RESULT 2
AAG77798
ID AAG77798 standard; protein; 396 AA.
XX AAG77798;
AC AAG77798;
XX 29-JAN-2002 (first entry)
DT Human EX33 G-protein coupled receptor polypeptide.
DE
XX G-protein coupled receptor; EX33; rheumatoid arthritis;
KW neutrophil-associated inflammatory disease; Crohn's disease;
KW ulcerative colitis; chronic obstructive pulmonary disease; COPD;
KW adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KW inflammatory bowel disease; human; GPCR.
XX
OS Homo sapiens.
XX
PN WO200166597-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-EP002462.
XX
PR 06-MAR-2000; 2000US-00518832.
XX
PA (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PI Jarai G, Cooper PR, Yousefi S;
XX WPI; 2001-541917/60.
DR N-PSDB; AAH78712.
XX
PT Use of an inflammatory related G-protein coupled receptor (EX33), a
PT polynucleotide encoding it or other compounds (e.g. antibodies) in the
PT diagnosis or treatment of a neutrophil-associated inflammatory disease,

PT e.g. rheumatoid arthritis.
XX
PS Claim 1; Page 29-30; 32pp; English.
XX
CC The present amino acid sequence represents EX33, a human inflammatory
CC disease-related G-protein coupled receptor (GPCR). G-protein coupled
CC receptors are important targets in therapeutic applications because they
CC are involved in a wide variety of physiological and pathological
CC processes. The invention comprises the use of the EX33 polypeptide and
CC polynucleotide in the diagnosis or treatment of a neutrophil-associated
CC inflammatory disease. The EX33 polypeptide, EX33 polynucleotide, an
CC antibody specific to the EX33 polypeptide, and an antisense
CC oligonucleotide/polynucleotide probe specific to the EX33 polynucleotide
CC are useful in the diagnosis or treatment of neutrophil-associated
CC inflammatory diseases, such as chronic obstructive pulmonary disease
CC (COPD), adult respiratory distress syndrome (ARDS), rheumatoid arthritis,
CC and inflammatory bowel diseases (e.g., Crohn's disease and ulcerative
CC colitis)
XX
SQ Sequence 396 AA;
Query Match 100.0%; Score 2041; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 1e-200;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNWSSDANFSCYHESVLGYRYVAVSWGVAVTGTVGNVLTLLALAIQPKLRTRENLIA 60
Db 1 MNWSSDANFSCYHESVLGYRYVAVSWGVAVTGTVGNVLTLLALAIQPKLRTRENLIA 60
QY 61 NLTADLLYCTLLQPFSSVDTYLHLHWTGATFCRVFGLLFASNSVSILTCLIALGRL 120
Db 61 NLTADLLYCTLLQPFSSVDTYLHLHWTGATFCRVFGLLFASNSVSILTCLIALGRL 120
QY 121 LIAHPKLPQVFSKAGIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSKAGIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQALDQYKLRQASIHNSHVARTDEAMPGRFQE 240
Db 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQALDQYKLRQASIHNSHVARTDEAMPGRFQE 240
QY 241 LDSRLASGGPSEGISSEPVSAATTQTLGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 300
Db 241 LDSRLASGGPSEGISSEPVSAATTQTLGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 300
QY 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNLTLDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNLTLDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVYAAMNRQFRQAYGSIKRGPRSFHRLH 396
Db 361 LNCINPVLVYAAMNRQFRQAYGSIKRGPRSFHRLH 396

RESULT 3
AAG80225
ID AAG80225 standard; protein; 396 AA.
XX AAG80225;
AC AAG80225;
XX 22-JAN-2002 (first entry)
DT Human MAR1 protein.
DE
XX MAR1; monoamine receptor-1; human; cytostatic; gene therapy; tumour;
KW psychiatric disorder; transgenic animal; knockout animal.
XX Homo sapiens.
OS
XX DE10021474-A1.
PN
XX 08-NOV-2001.
PD
XX

PF 03-MAY-2000; 2000DE-01021474.
XX
PR 03-MAY-2000; 2000DE-01021474.
XX
PA (BRUE/) BRUESS M.
PA (BOEN/) BOENISCH H.
XX
PI Bruess M, Boenisch H;
XX
XX WPI; 2002-011956/02.
DR N-PSDB; AAI68792, AAI68793.
XX
XX New monoamine receptor-1 gene, MAR1, useful for diagnosis and treatment
PT of MAR1-related diseases.
PT
XX
PS Disclosure; Page 4; 6pp; German.
XX
XX This invention describes a novel human monoamine receptor-1 (MAR1) gene
CC (I) which has cytostatic activity and can be used for gene therapy. (I),
CC and derived (anti)sense oligonucleotides, are useful in treatment and
CC diagnosis of (I)-related diseases (possibly tumours and psychiatric
CC disorders), for producing transgenic/knockout animals, and for
CC recombinant expression of the protein (II) that it encodes. (II) is
CC useful in ligand-binding studies and screening assays, also for treatment
CC and diagnosis of (II)-related diseases. This sequence represents the
CC human MAR1 monoamine receptor-1 protein
XX
XX Sequence 396 AA;
SQ
Query Match 100.0%; Score 2041; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 1e-200;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVNTLLALAIQPKLRTFNLLIA 60
Db 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVNTLLALAIQPKLRTFNLLIA 60
Qy 61 NLTLADLLYCTLLQPFSDVTYHLHWRTGATFCRVFGLLLFASNSVSILTLCLIALGRYL 120
Db 61 NLTLADLLYCTLLQPFSDVTYHLHWRTGATFCRVFGLLLFASNSVSILTLCLIALGRYL 120
Qy 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Qy 181 ILMGIYFVLGLSSVGIFYCLIHROVKRAAQALDQYKLRQASIHNSNHVARTDEAMPGRFQE 240
Db 181 ILMGIYFVLGLSSVGIFYCLIHROVKRAAQALDQYKLRQASIHNSNHVARTDEAMPGRFQE 240
Qy 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 300
Db 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 300
Qy 301 IKGARRAPDSSEFGKVTMCMFAVFLCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSEFGKVTMCMFAVFLCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
RESULT 4
ABP95618
ID ABP95618 standard; protein; 396 AA.
XX
AC ABP95618;
XX
DT 06-MAR-2003 (first entry)
XX
DE Human GPCR polypeptide SEQ ID NO 46.
XX
KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;

drug development; gustatory; taste; fragrance; receptor.
Homo sapiens.
WO200216548-A2.
28-FEB-2002.
30-JUL-2001; 2001WO-IB001446.
04-AUG-2000; 2000JP-00237818.
13-FEB-2001; 2001JP-00034434.
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA
XX Haga T, Takeda S, Mitaku S;
PI
XX WPI; 2002-304118/34.
DR N-PSDB; ABZ42892.
XX
XX Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.
XX
XX Claim 10; SEQ ID NO 46; 97pp + Sequence Listing; Japanese.
PS
XX The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 396 AA;
SQ
Query Match 100.0%; Score 2041; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 1e-200;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVNTLLALAIQPKLRTFNLLIA 60
Db 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVNTLLALAIQPKLRTFNLLIA 60
Qy 61 NLTLADLLYCTLLQPFSDVTYHLHWRTGATFCRVFGLLLFASNSVSILTLCLIALGRYL 120
Db 61 NLTLADLLYCTLLQPFSDVTYHLHWRTGATFCRVFGLLLFASNSVSILTLCLIALGRYL 120
Qy 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Qy 181 ILMGIYFVLGLSSVGIFYCLIHROVKRAAQALDQYKLRQASIHNSNHVARTDEAMPGRFQE 240
Db 181 ILMGIYFVLGLSSVGIFYCLIHROVKRAAQALDQYKLRQASIHNSNHVARTDEAMPGRFQE 240
Qy 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 300
Db 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 300
Qy 301 IKGARRAPDSSEFGKVTMCMFAVFLCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSEFGKVTMCMFAVFLCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
Qy 361 LNGCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNGCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 5
ABJ19755
ID ABJ19755 standard; protein; 396 AA.
XX
AC
XX
XX
DT 03-APR-2003 (first entry)
XX
DE Human MP21 protein EX33 SEQ ID No 35.
XX
KW Cytostatic; p21 pathway modulating agent; cancer; angiogenic; apoptotic;
KW cell proliferation disorder; MP21.
XX
OS Homo sapiens.
XX
XX
PN WO2003006990-A1.
XX
PD 23-JAN-2003.
XX
PF 10-JUL-2002; 2002WO-US021549.
XX
PR 12-JUL-2001; 2001US-0305017P.
PR 10-OCT-2001; 2001US-0328491P.
PR 15-FEB-2002; 2002US-0357452P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Li D, Funke RP;
XX
XX WPI; 2003-221779/21.
DR N-PSDB; ABT17029.
XX
PT Identifying candidate p21 pathway modulator, by contacting an assay
PT system having modifiers of p21 polypeptide or gene with a test agent to
PT provide a reference activity in system and detecting test agent-biased
PT activity.
XX
PS Example; Page 121-123; 199pp; English.
XX
CC The invention relates to a novel method for identifying a candidate p21
CC pathway modulating agent. The novel method comprises contacting an assay
CC system, comprising a purified MP21 polypeptide (modifier of p21) or
CC nucleic acid, with a test agent under conditions, so that but for the
CC presence of a test agent, the assay system provides a reference activity
CC and detection of test agent-biased activity of the assay system. The
CC novel method of the invention is useful for identifying a candidate p21
CC pathway modulating agent. The invention also includes a method for
CC modulating the p21 pathway of a cell, and a method for diagnosing a
CC disease e.g. cancer in a patient. The identified modulators are useful in
CC diagnosis, therapy and pharmaceutical development. The modulators are
CC useful in a variety of diagnostic and therapeutic applications including
CC angiogenic, apoptotic and cell proliferation disorders. This sequence
CC represents an MP21 protein of the invention
XX
SQ Sequence 396 AA;

Query Match 100.0%; Score 2041; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 1e-200;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSSDANFSCYHESVLGYRYVAVSVGVVAVTGVGNVLTLLALAIQPKLRTFRNLLIA 60
Db 1 MNSSDANFSCYHESVLGYRYVAVSVGVVAVTGVGNVLTLLALAIQPKLRTFRNLLIA 60
QY 61 NLTLADLLYCTLLQPFVSDTYLHLHWRGTATFCRVFGLLLFASNSVSILTLCLIALGRYL 120
Db 61 NLTLADLLYCTLLQPFVSDTYLHLHWRGTATFCRVFGLLLFASNSVSILTLCLIALGRYL 120
QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVSAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSAGKIVLALVSTWVGVSAPLWPIYILVPVCTCSFDRIRGRPYTT 180

QY 181 ILMGIYFVLGLSSVGIIFYCLIHROVKRAAALDQYKLRQASIHSHVARTDEAMPGRFOE 240
Db 181 ILMGIYFVLGLSSVGIIFYCLIHROVKRAAALDQYKLRQASIHSHVARTDEAMPGRFOE 240
QY 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVDQINSKRAQMAEKSPPEASAKAQP 300
Db 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVDQINSKRAQMAEKSPPEASAKAQP 300
QY 301 IKGARRAPDSSESEFGKVTMCFVFLCFALSYIPFLLNILDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSESEFGKVTMCFVFLCFALSYIPFLLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVYAMNROFRQAYGSILKRGPRSFHRLH 396
Db 361 LNCINPVLVYAMNROFRQAYGSILKRGPRSFHRLH 396

RESULT 6
ABP81705
ID ABP81705 standard; protein; 396 AA.
XX
AC ABP81705;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human G protein-coupled receptor EX33 protein SEQ ID NO:585.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
XX WPI; 2003-046718/04.
DR N-PSDB; ABZ42551.

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, memory
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 396 AA;

Query Match 100.0%; Score 2041; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 1e-200;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALAIQPKLRTFRNLLIA 60
Db 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALAIQPKLRTFRNLLIA 60
QY 61 NLTADLLYCTLLQPFSDVTYHLHWRTGATFCRVFGLLPASNSVSILTCLIALGRYL 120
Db 61 NLTADLLYCTLLQPFSDVTYHLHWRTGATFCRVFGLLPASNSVSILTCLIALGRYL 120
QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSAGKIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFOE 240
Db 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFOE 240
QY 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
Db 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
QY 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNGCINPVLAAAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNGCINPVLAAAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 7
ABB82500
ID ABB82500 standard; protein; 396 AA.
XX
AC ABB82500;
XX
DT 22-JAN-2003 (first entry)
XX
DE Human TGR35 polypeptide.
XX
KW G-protein coupled receptor; GPCR; antipsoriatic; antiinflammatory;
KW antilipemic; nootropic; neuroprotective; antianemic; antiulcer; human;
KW antiparkinsonian; antilipemic; TGR35; receptor.
XX
OS Homo sapiens.
XX
PN WO200277001-A2.
XX
PD 03-OCT-2002.
XX
PF 08-MAR-2002; 2002WO-US007171.
XX

PR 09-MAR-2001; 2001US-00802803.
PR 16-MAR-2001; 2001US-0276649P.
XX
PA (TULA-) TULARIK INC.
XX
PI Tian H, Zhao J, Chen J, Cutler G;
XX
DR WPI; 2003-018881/01.
DR N-PSDB; ABV73365.
XX
PT New G-protein coupled receptor polypeptides and polynucleotides useful
PT for identifying compounds for treating a TGR-associated disorder, e.g.
PT psoriasis, inflammatory bowel disease, hyperlipidemia, Parkinson's
PT disease, anemia.
XX
PS Example 1; Page 64; 87pp; English.
XX
CC The invention relates to G-protein coupled receptor (GPCR) polypeptides
CC and encoding polynucleotides selected from TGR20, TGR35, TGR36, TGR183,
CC TGR341, TGR211, TGR216 and TGR79. The polypeptides and nucleic acids are
CC useful for identifying compounds for treating a TGR-associated disorder,
CC such as psoriasis, inflammatory bowel disease, hyperlipidemia,
CC Parkinson's disease, Huntington's disease, anemia, immune and blood
CC disorders, ulcerative colitis, Crohn's disease or spleen enlargement.
CC They are also useful for identifying cells such as kidney, liver,
CC hypothalamus, colon, adipose, or spleen cells, for forensics and
CC paternity determination, diagnosing diseases and examining signal
CC transduction. The present sequence represents a human TGR35 polypeptide
XX
SQ Sequence 396 AA;

Query Match 100.0%; Score 2041; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 1e-200;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALAIQPKLRTFRNLLIA 60
Db 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALAIQPKLRTFRNLLIA 60
QY 61 NLTADLLYCTLLQPFSDVTYHLHWRTGATFCRVFGLLPASNSVSILTCLIALGRYL 120
Db 61 NLTADLLYCTLLQPFSDVTYHLHWRTGATFCRVFGLLPASNSVSILTCLIALGRYL 120
QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSAGKIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFOE 240
Db 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFOE 240
QY 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
Db 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
QY 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNGCINPVLAAAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNGCINPVLAAAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 8
ABB82422
ID ABR62422 standard; protein; 396 AA.
XX
AC ABR62422;
XX
DT 03-OCT-2003 (first entry)
XX
DE Human hpl5a orphan G-protein coupled receptor.

XX Human; hp15a; receptor; G-protein coupled receptor; cardiant; gastrointestinal.
KW
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
FT Modified-site 3 /note= "potential N-glycosylation site"
FT Modified-site 8 /note= "potential N-glycosylation site"
FT Domain 20. .46
FT Domain 57. .79
FT Domain /note= "Transmembrane domain 1"
FT Domain /note= "Transmembrane domain 2"
FT Domain 95. .116
FT Domain /note= "Transmembrane domain 3"
FT Domain 137. .158
FT Domain /note= "Transmembrane domain 4"
FT Domain 183. .205
FT Domain /note= "Transmembrane domain 5"
FT Domain 315. .338
FT Domain /note= "Transmembrane domain 6"
FT Domain 351. .373
FT Domain /note= "Transmembrane domain 7"

WO2003054540-A1.

03-JUL-2003.

19-DEC-2002; 2002WO-US040612.

19-DEC-2001; 2001US-00029436.

(SYNA-) SYNAPTIC PHARM CORP.

Smith KE, Weinshank R;

WPI; 2003-559173/52.

N-PSDB; ACC84331.

New recombinant nucleic acid, useful for preparing a composition for treating disorders linked to human hp15a receptor e.g. cardiovascular or gastrointestinal disorders.

Disclosure; Fig 2A-C; 98pp; English.

The present sequence is the protein sequence of a novel human orphan G-protein coupled receptor, designated hp15a. The endogenous ligand for hp15a is likely to be a neuromodulator since the receptor is present in several regions of the human brain. The invention provides hp15a nucleic acids, vectors, host cells, antibodies, probes, antisense oligonucleotides, transgenic non-human animals, methods of isolating the receptor, methods of treating an abnormality that is associated with activity of hp15a e.g. cardiovascular or gastrointestinal disorders, and methods of determining binding of compounds to hp15a

Sequence 396 AA;

Query Match 100.0%; Score 2041; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 1e-200;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNWSSDANFSCYHESVLGVRVAVSVGWVAVTGTGVNLTLLALAIQPKLRTFRLIA 60

DB 1 MNWSSDANFSCYHESVLGVRVAVSVGWVAVTGTGVNLTLLALAIQPKLRTFRLIA 60

QY 61 NLTLADLLYCTLLQPFSDTYLHLHWRTGATFCRVGLLTFASNSVSLTLCIALGRYL 120

DB 61 NLTLADLLYCTLLQPFSDTYLHLHWRTGATFCRVGLLTFASNSVSLTLCIALGRYL 120

QY 121 LIAHPKLFPPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180

DB 121 LIAHPKLFPPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAQAALDQYKLRQASIHNSHNHVARTEAMPGRFQE 240
DB 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAQAALDQYKLRQASIHNSHNHVARTEAMPGRFQE 240
QY 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVDQINSKRAKQMAEKSPPEASAKAQ 300
DB 241 LDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVDQINSKRAKQMAEKSPPEASAKAQ 300
QY 301 IKGARRAPDSSESSEFGKVTMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360
DB 301 IKGARRAPDSSESSEFGKVTMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVAAMNRQFRQAYGSILKKGPRSFHRLH 396
DB 361 LNCINPVLVAAMNRQFRQAYGSILKKGPRSFHRLH 396

RESULT 9

AAM99936

ID AAM99936 standard; protein; 404 AA.

AC AAM99936;

XX

DT 04-JAN-2002 (first entry)

XX Human expressed polypeptide SEQ ID NO 60.

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.

XX Homo sapiens.

OS

XX WO200155387-A1.

PN

XX

XX

PD 02-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US001310.

XX

PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465573/50.
XX N-PSDB; AAI99548.
PT Isolated digestive system associated polypeptide for treating, preventing
PT and/ or prognosing disorders related to the digestive system including
PT digestive system cancers and also for testing and detection e.g.
PT diagnosis.
XX Claim 11; SEQ ID NO 60; 509pp + Sequence Listing; English.
PS The invention relates to novel genes (AAI99548-AAI99604) and proteins
XX (AAM99936-AAM99984) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 404 AA;

Query Match 100.0%; Score 2041; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.1e-200;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTVGNVTLTLLALAIQPKLRTRENFLLIA 60
Db 9 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTVGNVTLTLLALAIQPKLRTRENFLLIA 68
QY 61 NLTADLLYCTLLQPFSSVDTYLHLHWRTGATFCRVFGLLTFASNSVSILTCLIALGRYL 120
Db 69 NLTADLLYCTLLQPFSSVDTYLHLHWRTGATFCRVFGLLTFASNSVSILTCLIALGRYL 128
QY 121 LIAHPKLPQVFSAGKIVLALVSTVWVGVSFAPLWPIYILVPVVTCTSFDRIRGRPYTT 180
Db 129 LIAHPKLPQVFSAGKIVLALVSTVWVGVSFAPLWPIYILVPVVTCTSFDRIRGRPYTT 188
QY 181 ILMGIFYVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHNVARTDEAMPGRFQE 240
Db 189 ILMGIFYVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHNVARTDEAMPGRFQE 248
QY 241 LDSRLASGGPSEGISSEPVSAATTQLEGDSSEVGDDQINSKRAKQMAEKSPPEASAKAQP 300
Db 249 LDSRLASGGPSEGISSEPVSAATTQLEGDSSEVGDDQINSKRAKQMAEKSPPEASAKAQP 308
QY 301 IKGARRAPDSSEFGKVTMCFVAVLFCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
Db 309 IKGARRAPDSSEFGKVTMCFVAVLFCFALSYPFLLNILDARVQAPRVVHMLAANLTW 368
QY 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 369 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 404

RESULT 10
ABB82509
ID ABB82509 standard; protein; 396 AA.

XX AC ABB82509;
XX DT 22-JAN-2003 (first entry)
XX DE Mouse TGR35 polypeptide.

XX KW G-protein coupled receptor; GPCR; antipsoriatic; antiinflammatory;
KW antilipemic; nootropic; neuroprotective; antianemic; antiulcer; mouse;
KW antiparkinsonian; antilipemic; TGR35; receptor.

XX OS Mus sp.
XX PN WO200277001-A2.
XX PD 03-OCT-2002.
XX PF 08-MAR-2002; 2002WO-US007171.
XX PR 09-MAR-2001; 2001US-00802803.
XX PR 16-MAR-2001; 2001US-0276649P.
XX PA (TULA-) TULARIK INC.

XX PI Tian H, Zhao J, Chen J, Cutler G;
XX DR WPI; 2003-018881/01.
XX DR N-PSDB; ABV73374.

XX PT New G-protein coupled receptor polypeptides and polynucleotides useful
PT for identifying compounds for treating a TGR-associated disorder, e.g.
PT psoriasis, inflammatory bowel disease, hyperlipidemia, Parkinson's
PT disease, anemia.

XX PS Claim 53; Page 71; 87pp; English.

XX CC The invention relates to G-protein coupled receptor (GPCR) polypeptides
CC and encoding polynucleotides selected from TGR20, TGR35, TGR36, TGR183,
CC TGR341, TGR211, TGR216 and TGR79. The polypeptides and nucleic acids are
CC useful for identifying compounds for treating a TGR-associated disorder,

CC such as psoriasis, inflammatory bowel disease, hyperlipidemia,
CC Parkinson's disease, Huntington's disease, anemia, immune and blood
CC disorders, ulcerative colitis, Crohn's disease or spleen enlargement.
CC They are also useful for identifying cells such as kidney, liver,
CC hypothalamus, colon, adipose, or spleen cells, for forensics and
CC paternity determination, diagnosing diseases and examining signal
CC transduction. The present sequence represents a mouse TGR35 polypeptide
XX Sequence 396 AA;
SQ

Query Match 85.6%; Score 1748; DB 6; Length 396;
Best Local Similarity 85.4%; Pred. No. 1.4e-170;
Matches 338; Conservative 20; Mismatches 38; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTVGNVTLTLLALAIQPKLRTRENFLLIA 60
Db 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTVGNVTLTLLALAIQPKLRTRENFLLIA 60
QY 61 NLTADLLYCTLLQPFSSVDTYLHLHWRTGATFCRVFGLLTFASNSVSILTCLIALGRYL 120
Db 61 NLTADLLYCTLLQPFSSVDTYLHLHWRTGATFCRVFGLLTFASNSVSILTCLIALGRYL 120
QY 121 LIAHPKLPQVFSAGKIVLALVSTVWVGVSFAPLWPIYILVPVVTCTSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSAGKIVLALVSTVWVGVSFAPLWPIYILVPVVTCTSFDRIRGRPYTT 180
QY 181 ILMGIFYVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHNVARTDEAMPGRFQE 240
Db 181 ILMGIFYVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHNVARTDEAMPGRFQE 240
QY 241 LDSRLASGGPSEGISSEPVSAATTQLEGDSSEVGDDQINSKRAKQMAEKSPPEASAKAQP 300
Db 241 LDSRLASGGPSEGISSEPVSAATTQLEGDSSEVGDDQINSKRAKQMAEKSPPEASAKAQP 300
QY 301 IKGARRAPDSSEFGKVTMCFVAVLFCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
Db 301 TAGARRATDAPSEFGKVTMCFVAVLFCFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 11
AAM87595
ID AAM87595 standard; protein; 115 AA.

XX AC AAM87595;
XX DT 07-NOV-2001 (first entry)

XX DE Human immune/haematopoietic antigen SEQ ID NO:15188.

XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.

XX OS Homo sapiens.

XX PN WO200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001354.

XX PR 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184664P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226682P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

N-PSDB; AAK60376.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Claim 11; SEQ ID NO 15188; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) CC proteins, and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased

CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 115 AA;

Query Match 27.9%; Score 570; DB 4; Length 115;
 Best Local Similarity 99.1%; Pred. No. 2.9e-50;
 Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 213 DQYKLRQASIHNSHVARTDEMPGRFQELDSRLASGSGISSEPVSAATTQLEGDSS 272
 Db 1 DQYKLRQASIHNSHVARTDEMPGRFQELDSRLASGSGISSEPVSAATTQLEGDSS 60
 QY 273 EVGDIQNSKRAKQMAEKSPPEASAKAQPIKGARRAPDSSEFGKVTMCFVFLC 327
 Db 61 EVGDIQNSKRAKQMAEKSPPEASAKAQPIKGARRAPDSSEFGKVTMCFVFLC 115

RESULT 12
 ABB89377
 ID ABB89377 standard; protein; 124 AA.
 XX
 AC ABB89377;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 1753.
 XX
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200190304-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-US016450.
 XX
 PR 19-MAY-2000; 2000US-0205515P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-122018/16.
 DR N-PSDB; ABL89786.
 XX
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 1753; 2081pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and

CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 124 AA;

Query Match 27.8%; Score 568; DB 5; Length 124;
 Best Local Similarity 98.2%; Pred. No. 5.2e-50;
 Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNNVTLALAIQPKLRTRENLLIA 60
 Db 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNNVTLALAIQPKLRTRENLLIA 60
 QY 61 NLTLADLLYCTLLQPFVSVDVTLHLHWRGTATFCRVFGLLLFASNSVSILTLC 112
 Db 61 NLTLADLLYCTLLQPFVSVDVTLHLHWRGTATFCRVFGLLLFASNSVSILTLC 112

RESULT 13
 AAU18097
 ID AAU18097 standard; protein; 116 AA.
 XX
 AC AAU18097;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Novel human uterine motility-association polypeptide #4.
 XX
 KW Human; uterine motility-association disorder; uterus; pregnancy; labour;
 KW menstrual cycle; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200155201-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001317.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PI Rosen CA, Barash SC, Ruben SM;

XX
DR WPI; 2001-488777/53.
DR N-PSDB; AAS28939.

PT New nucleic acid molecules encoding 49 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.

XX
PS Claim 11; SEQ ID NO 73; 524pp; English.

XX
CC The present invention relates to the isolation of novel human uterine
CC motility-association polypeptides, and cDNA (AAS28936-AAS28994) and
CC genomic sequences encoding for these polypeptides. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with uterine motility such as pregnancy
CC and labour, and menstrual disorders. The polynucleotide sequences of the
CC invention are also useful in gene therapy. AAU18094-AAU18152 represent
CC novel human uterine motility-association polypeptides. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 116 AA;

Query Match 22.2%; Score 454; DB 4; Length 116;

Best Local Similarity 98.9%; Pred. No. 2.5e-38;

Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNSSDANFSCYHESVLGYRYAVSWGVVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 60

Db 9 MNSSDANFSCYHESVLGYRYAVSWGVVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 68

QY 61 NLTLDLCTLLQPFSDTYLHLHRT 88
Db 69 NLTLDLCTLLQPFSDTYLHLXWRT 96

RESULT 14
AAU18646
ID AAU18646 standard; protein; 116 AA.
XX AC AAU18646;
XX DT 21-NOV-2001 (first entry)
XX DE Renal and cardiovascular-associated protein, Seq ID 85.
XX KW Human; antiinflammatory; neuroprotective; immunomodulator; vulnary;
KW cardiovascular; cytostatic; nephrotropic; antianaemic; nephritis;
KW immunosuppressive; kidney disorder; renal failure; hypertension;
KW cardiovascular disorder; myocardial infarction; blood disorder; anaemia;
KW blood coagulation disorder; electrolyte imbalance disorder; cancer;
KW hyponatraemia; hyperkalaemia; neoplastic disorder; nephroma;
KW autoimmune disease; inflammatory disease; reproductive system disorder;
KW endocrine disorder; neural activity; neurological disorder;
KW wound healing; respiratory disorder.

OS Homo sapiens.

XX PN WO20015328-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001359.

XX PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-488787/53.
N-PSDB; AAS30167.

New polynucleotides and polypeptides, useful for diagnosing, treating, preventing or prognosing e.g. kidney, cardiovascular, blood, electrolyte imbalance or neoplastic disorders, autoimmune diseases, cancers.

Claim 1; SEQ ID NO 85; 506pp; English.

The invention relates to novel nucleic acids and polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to these polypeptides. The polynucleotides are especially useful in the diagnosis, prognosis, prevention and/or treatment of diseases which include kidney disorders (e.g. renal failure or nephritis), cardiovascular disorders (e.g. hypertension or myocardial infarction), blood disorders (e.g. anaemia or blood coagulation disorders), electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia), neoplastic disorders (e.g. nephroma or renal cell cancer), autoimmune diseases, cancers, inflammatory diseases, reproductive system disorders, endocrine disorders, neural activity and neurological disorders, wound healing and respiratory disorders. AAU18644-AAU18715 represent the novel human renal and cardiovascular-associated amino acid sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences

Sequence 116 AA;

Query Match 22.2%; Score 454; DB 4; Length 116;
Best Local Similarity 98.9%; Pred. No. 2.5e-38;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSGVVAVTGTGNNVLTLLALAIQPKLRTRENLIIA 60
DB 9 MNSSDANFSCYHESVLGYRYVAVSGVVAVTGTGNNVLTLLALAIQPKLRTRENLIIA 68
QY 61 NLTLADLLYCTLLQPFSDVDTYHLHWRM 88
DB 69 NLTLADLLYCTLLQPFSDVDTYHLXWRT 96

RESULT 15
AAU21583
ID AAU21583 standard; protein; 116 AA.

XX AAU21583;
AC
XX
DT 06-DEC-2001 (first entry)
XX
DE Novel human neoplastic disease associated polypeptide #16.
XX
KW Human; neoplastic disease associated polypeptide; cancer;
KW hyperproliferative disorder; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic.
XX Homo sapiens.
XX
PN WO200155163-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001358.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225477P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.

Search completed: September 24, 2004, 08:36:35
Job time : 137 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 08:39:32 ; Search time 413 Seconds
(without alignments)
308.323 Million cell updates/sec

Title: US-10-029-436-2
Perfect score: 2041
Sequence: 1 MNWSSDANFSCYHESVLGYR.....FRQAYGSILKGRPSFRLH 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues
Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2041	100.0	396	9 US-09-826-508-38	Sequence 38, Appl
2	2041	100.0	396	9 US-09-798-710-2	Sequence 2, Appli
3	2041	100.0	396	12 US-10-343-650A-46	Sequence 46, Appl
4	2041	100.0	396	14 US-10-094-417-4	Sequence 4, Appli
5	2041	100.0	396	14 US-10-225-567A-585	Sequence 585, App
6	2041	100.0	396	14 US-10-029-436-2	Sequence 2, Appli
7	2041	100.0	404	14 US-10-073-885-60	Sequence 60, Appl
8	1748	85.6	396	14 US-10-094-417-22	Sequence 22, Appl
9	1168	57.2	310	14 US-10-017-161-1922	Sequence 1922, Ap
10	568	27.8	124	15 US-10-264-237-1753	Sequence 1753, Ap
11	454	22.2	116	9 US-09-764-853-482	Sequence 482, App
12	454	22.2	116	10 US-09-989-442-85	Sequence 85, Appl
13	454	22.2	116	10 US-09-764-886-60	Sequence 60, Appl
14	454	22.2	116	11 US-09-764-875-641	Sequence 641, App
15	454	22.2	116	12 US-09-764-886-60	Sequence 60, Appl

16	454	22.2	116	12	US-09-764-893-73	Sequence 73, Appl
17	454	22.2	116	14	US-10-073-865-73	Sequence 73, Appl
18	454	22.2	116	14	US-10-103-313-310	Sequence 310, App
19	454	22.2	116	14	US-10-073-885-87	Sequence 87, Appl
20	338	16.6	386	14	US-10-270-333-18	Sequence 18, Appl
21	290.5	14.2	515	14	US-10-238-129-10	Sequence 10, Appl
22	290.5	14.2	515	14	US-10-238-667-10	Sequence 10, Appl
23	290	14.2	443	14	US-10-060-795B-11	Sequence 11, Appl
24	290	14.2	443	14	US-10-157-031-78	Sequence 78, Appl
25	290	14.2	443	14	US-10-225-567A-102	Sequence 102, App
26	290	14.2	443	15	US-10-352-684A-2	Sequence 2, Appli
27	290	14.2	445	15	US-10-292-798-658	Sequence 658, App
28	288.5	14.1	466	10	US-09-992-238-19	Sequence 19, Appl
29	288.5	14.1	466	15	US-10-436-715-45	Sequence 45, Appl
30	288.5	14.1	497	13	US-10-052-589-2	Sequence 2, Appli
31	287.5	14.1	515	14	US-10-238-129-9	Sequence 9, Appli
32	287.5	14.1	515	14	US-10-238-667-9	Sequence 9, Appli
33	286.5	14.0	517	9	US-09-951-622-10	Sequence 10, Appl
34	286.5	14.0	517	14	US-10-325-930-10	Sequence 10, Appl
35	286.5	14.0	592	15	US-10-369-493-6772	Sequence 6772, Ap
36	285.5	14.0	520	14	US-10-185-991-4	Sequence 4, Appli
37	285.5	14.0	520	14	US-10-238-129-4	Sequence 4, Appli
38	285.5	14.0	520	14	US-10-238-667-4	Sequence 4, Appli
39	285.5	14.0	520	14	US-10-225-567A-36	Sequence 36, Appl
40	285	14.0	443	11	US-09-826-509-489	Sequence 489, App
41	283.5	13.9	462	14	US-10-017-161-754	Sequence 754, App
42	283.5	13.9	515	14	US-10-054-616A-2	Sequence 2, Appli
43	283.5	13.9	515	14	US-10-054-616A-4	Sequence 4, Appli
44	283.5	13.9	515	14	US-10-054-616A-5	Sequence 5, Appli
45	283.5	13.9	515	16	US-10-633-438-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-826-508-38
; Sequence 38, Application US/09826508
; Patent No. US20010025099A1
; GENERAL INFORMATION:
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Lisa Vawter
; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
; TITLE OF INVENTION: and Polynucleotides
; FILE REFERENCE: GP-70744USB
; CURRENT APPLICATION NUMBER: US/09/826,508
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 396
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-826-508-38

Query Match		100.0%;	Score 2041;	DB 9;	Length 396;
Best Local Similarity		100.0%;	Pred. No. 1.5e-187;		
Matches 396;		Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	1	MNWS	DANFSCYHESVLGYRYAVSWG	VVAVTGT	GVNVLTLALAIQPKLRTFRNLLIA 60
Db	1	MNWS	DANFSCYHESVLGYRYAVSWG	VVAVTGT	GVNVLTLALAIQPKLRTFRNLLIA 60
QY	61	NLT	LADLLYCTLLQPF	SVDTYTLHLHWR	TGATFCRVFGLLLFASNSVSILTLCLIALGRYL 120
Db	61	NLT	LADLLYCTLLQPF	SVDTYTLHLHWR	TGATFCRVFGLLLFASNSVSILTLCLIALGRYL 120
QY	121	LIA	HPKLFPPQVFS	AKGIVLALVSTWV	GVASAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db	121	LIA	HPKLFPPQVFS	AKGIVLALVSTWV	GVASAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY	181	ILM	GIYFVLGLSSVGI	FYCLIH	RQVKRAQAQALDQYKLRQASIHNSHNHARTDEAMPGRFQE 240
Db	181	ILM	GIYFVLGLSSVGI	FYCLIH	RQVKRAQAQALDQYKLRQASIHNSHNHARTDEAMPGRFQE 240

Db 181 ILMGIYFVLGLSSVGIFYCLIHQVKKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFOE 240
QY 241 LDSRLASGGPSEGISSEPVSAATQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
Db 241 LDSRLASGGPSEGISSEPVSAATQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
QY 301 IKGARRAPDSSEFGKVTMCFVAVLQFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSEFGKVTMCFVAVLQFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 2

US-09-798-710-2
; Sequence 2, Application US/09798710
; Publication No. US20020187947A1
; GENERAL INFORMATION:
; APPLICANT: Jarai, Gabor
; APPLICANT: Cooper, Paul Roy
; APPLICANT: Yousefi, Shida
; TITLE OF INVENTION: No. US20020187947A1e1 Gene
; FILE REFERENCE: 4-31328A/H026
; CURRENT APPLICATION NUMBER: US/09/798,710
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/XXX,XXX
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-710-2

Query Match 100.0%; Score 2041; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNNVLTLLALAIQPKLRTRFNLLIA 60
Db 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNNVLTLLALAIQPKLRTRFNLLIA 60
QY 61 NLTLADLLYCTLLQPFSDVTYHLHWRGTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
Db 61 NLTLADLLYCTLLQPFSDVTYHLHWRGTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY 181 ILMGIYFVLGLSSVGIFYCLIHQVKKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFOE 240
Db 181 ILMGIYFVLGLSSVGIFYCLIHQVKKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFOE 240
QY 241 LDSRLASGGPSEGISSEPVSAATQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
Db 241 LDSRLASGGPSEGISSEPVSAATQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
QY 301 IKGARRAPDSSEFGKVTMCFVAVLQFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSEFGKVTMCFVAVLQFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 3

US-10-343-650A-46
; Sequence 46, Application US/10343650A

; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-46

Query Match 100.0%; Score 2041; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNNVLTLLALAIQPKLRTRFNLLIA 60
Db 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNNVLTLLALAIQPKLRTRFNLLIA 60
QY 61 NLTLADLLYCTLLQPFSDVTYHLHWRGTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
Db 61 NLTLADLLYCTLLQPFSDVTYHLHWRGTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY 181 ILMGIYFVLGLSSVGIFYCLIHQVKKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFOE 240
Db 181 ILMGIYFVLGLSSVGIFYCLIHQVKKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFOE 240
QY 241 LDSRLASGGPSEGISSEPVSAATQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
Db 241 LDSRLASGGPSEGISSEPVSAATQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
QY 301 IKGARRAPDSSEFGKVTMCFVAVLQFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSEFGKVTMCFVAVLQFALSYPFLLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 4

US-10-094-417-4
; Sequence 4, Application US/10094417
; Publication No. US20030045685A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030045685A1e1 Receptors
; FILE REFERENCE: 018781-008110US
; CURRENT APPLICATION NUMBER: US/10/094,417
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/802,803
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/276,649
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4

```

; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR35
US-10-094-417-4
Query Match      100.0%; Score 2041; DB 14; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALAIQPKLRTFRNLLIA 60
Db      1  MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALAIQPKLRTFRNLLIA 60

QY      61  NLTLADLLYCTLLQPFSDVTYLHLHWRTGATFCRVFGLLLFASNVSILTCLIALGRYL 120
Db      61  NLTLADLLYCTLLQPFSDVTYLHLHWRTGATFCRVFGLLLFASNVSILTCLIALGRYL 120

QY      121  LIAHPKLFPQVFSAGKIVLALVSTVWVGAFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db      121  LIAHPKLFPQVFSAGKIVLALVSTVWVGAFAPLWPIYILVPVCTCSFDRIRGRPYTT 180

QY      181  ILMGIYFVLGLSSVGIFYCLIHROVKRAAQAALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
Db      181  ILMGIYFVLGLSSVGIFYCLIHROVKRAAQAALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240

QY      241  LDSRLASGGPSEGISSEPVSAAATTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
Db      241  LDSRLASGGPSEGISSEPVSAAATTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300

QY      301  IKGARRAPDSSESEFGKVTRMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360
Db      301  IKGARRAPDSSESEFGKVTRMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360

QY      361  LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396
Db      361  LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 5
US-10-225-567A-585
; Sequence 585, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225.567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 585
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-585
Query Match      100.0%; Score 2041; DB 14; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALAIQPKLRTFRNLLIA 60
Db      1  MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALAIQPKLRTFRNLLIA 60

QY      61  NLTLADLLYCTLLQPFSDVTYLHLHWRTGATFCRVFGLLLFASNVSILTCLIALGRYL 120
Db      61  NLTLADLLYCTLLQPFSDVTYLHLHWRTGATFCRVFGLLLFASNVSILTCLIALGRYL 120
```

```

Db      61  NLTLADLLYCTLLQPFSDVTYLHLHWRTGATFCRVFGLLLFASNVSILTCLIALGRYL 120
QY      121  LIAHPKLFPQVFSAGKIVLALVSTVWVGAFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db      121  LIAHPKLFPQVFSAGKIVLALVSTVWVGAFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY      181  ILMGIYFVLGLSSVGIFYCLIHROVKRAAQAALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
Db      181  ILMGIYFVLGLSSVGIFYCLIHROVKRAAQAALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
QY      241  LDSRLASGGPSEGISSEPVSAAATTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
Db      241  LDSRLASGGPSEGISSEPVSAAATTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
QY      301  IKGARRAPDSSESEFGKVTRMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360
Db      301  IKGARRAPDSSESEFGKVTRMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360
QY      361  LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396
Db      361  LNCINPVLVYAAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 6
US-10-029-436-2
; Sequence 2, Application US/10029436
; Publication No. US20030124138A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E.
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA Encoding A Human Receptor (hpl5a) And Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 55180
; CURRENT APPLICATION NUMBER: US/10/029,436
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US/09/179,798A
; PRIOR FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-436-2
Query Match      100.0%; Score 2041; DB 14; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALAIQPKLRTFRNLLIA 60
Db      1  MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALAIQPKLRTFRNLLIA 60

QY      61  NLTLADLLYCTLLQPFSDVTYLHLHWRTGATFCRVFGLLLFASNVSILTCLIALGRYL 120
Db      61  NLTLADLLYCTLLQPFSDVTYLHLHWRTGATFCRVFGLLLFASNVSILTCLIALGRYL 120

QY      121  LIAHPKLFPQVFSAGKIVLALVSTVWVGAFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db      121  LIAHPKLFPQVFSAGKIVLALVSTVWVGAFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY      181  ILMGIYFVLGLSSVGIFYCLIHROVKRAAQAALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
Db      181  ILMGIYFVLGLSSVGIFYCLIHROVKRAAQAALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
QY      241  LDSRLASGGPSEGISSEPVSAAATTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
Db      241  LDSRLASGGPSEGISSEPVSAAATTQLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
QY      301  IKGARRAPDSSESEFGKVTRMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360
Db      301  IKGARRAPDSSESEFGKVTRMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360
```

QY 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 7

US-10-073-885-60
; Sequence 60, Application US/10073885
; Publication No. US20030096346A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ03C1
; CURRENT APPLICATION NUMBER: US/10/073,885
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-073-885-60

Query Match 100.0%; Score 2041; DB 14; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNWSSDANFSCYHESVLGYRYVAVSWGVTGTVGNVLTLLALAIQPKLRTRENLLIA 60
Db 9 MNWSSDANFSCYHESVLGYRYVAVSWGVTGTVGNVLTLLALAIQPKLRTRENLLIA 68
QY 61 NLTADLLYCTLLQPFSSVDTYLHLHWTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
Db 69 NLTADLLYCTLLQPFSSVDTYLHLHWTGATFCRVFGLLLFASNSVSILTCLIALGRYL 128
QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 129 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 188
QY 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFQE 240
Db 189 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFQE 248
QY 241 LDSRLASGGPSEGISSEPVSAATQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 300
Db 249 LDSRLASGGPSEGISSEPVSAATQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 308
QY 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNILDARVQAPRVVHMLAANLTW 360
Db 309 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNILDARVQAPRVVHMLAANLTW 368
QY 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 369 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 404

RESULT 8

US-10-094-417-22
; Sequence 22, Application US/10094417
; Publication No. US20030045685A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: NO. US20030045685A1e1 Receptors
; FILE REFERENCE: 018781-008110US

; CURRENT APPLICATION NUMBER: US/10/094,417
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/802,803
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/276,649
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) TGR35
US-10-094-417-22

Query Match 85.6%; Score 1748; DB 14; Length 396;
Best Local Similarity 85.4%; Pred. No. 2.4e-159;
Matches 338; Conservative 20; Mismatches 38; Indels 0; Gaps 0;

QY 1 MNWSSDANFSCYHESVLGYRYVAVSWGVTGTVGNVLTLLALAIQPKLRTRENLLIA 60
Db 1 MNWSSDANFSCYHESVLGYRYVAVSWGVTGTVGNVLTLLALAIQPKLRTRENLLIA 60
QY 61 NLTADLLYCTLLQPFSSVDTYLHLHWTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
Db 61 NLTADLLYCTLLQPFSSVDTYLHLHWTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
QY 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFQE 240
Db 181 ILMGIYFVLGLSSVGIFYCLIHQVKRAAQAALDQYKLRQASIHNSHVARTDEAMPGRFQE 240
QY 241 LDSRLASGGPSEGISSEPVSAATQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 300
Db 241 LDSRLASGGPSEGISSEPVSAATQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQ 300
QY 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNILDARVQAPRVVHMLAANLTW 360
Db 301 TAGARRATDAPSEFGKVTMCFVFLCFALSYPFLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396

RESULT 9

US-10-017-161-1922
; Sequence 1922, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1922
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (20)...(53)


```

; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (66)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (289)
; OTHER INFORMATION: Variable amino acid
US-10-017-161-1922

Query Match      57.2%; Score 1168; DB 14; Length 310;
Best Local Similarity 94.2%; Pred. No. 1.2e-103;
Matches 226; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 153 APLWPIYILVPVVCSCFDRIRGRPYTTILMGIYFVLGLSSVGIFYCLIHROVKRAAQAAL 212
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 70 APLWPIYILVPVVCRCWRDRIQSRPYTTILMGIYFVLGLSSVGIFYCLIHROVKRAAQAAL 129

QY 213 DQYKLRQASIHNSHVARTDEAMPGRFOELDSRLASGGPSEGISSEPVSAATTQTLEGDSS 272
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 DQYKLRQASVHSNHVARTDEAMPGRFOELDSRLASGGPSEGISSEPVSAATTQTLEGDSS 189

QY 273 EVGQINSKRAKQMAEKSPPEASAKAQPIKGARRAPDSSESSEFGKVTMCFVFLCFALSY 332
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 190 EVGQINSKRAKQMAEKSPPEASAKAQPIKGARRAPDSSESSEFGKVTMCFVFLCFALSY 249

QY 333 IPFLLNLILDARVQAPRVVHMLAANLTWLNCGINPVLVYAMNRQFRQAYGSILKRGPRSF 392
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 250 IPFLLNLILDARVQAPRVVHMLAANLTWLNCGINPVLVYAMNRQFRQAYGLLFFKRAPEF 309

RESULT 10
US-10-264-237-1753
; Sequence 1753, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1753
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (85)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1753

Query Match      27.8%; Score 568; DB 15; Length 124;
Best Local Similarity 98.2%; Pred. No. 1.8e-46;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MWNSSDANFSCYHESVLGYRYVAVSWGVTGTVGNVLTLLALAIQPKLRTFRNLLIA 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MWNSSDANFSCYHESVLGYRYVAVSWGVTGTVGNVLTLLALAIQPKLRTFRNLLIA 60

QY 61 NLTADLLCYTLQPFSDTYLHLHWRTGTCRFFVGLLLFASNSVSILTLC 112
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NLTADLLCYTLQPFSDTYLHLXWRTGTCRFFVGLLLFASNSVSILTLC 112
```

```

RESULT 11
US-09-764-853-482
; Sequence 482, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 482
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-482

Query Match      22.2%; Score 454; DB 9; Length 116;
Best Local Similarity 98.9%; Pred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MWNSSDANFSCYHESVLGYRYVAVSWGVTGTVGNVLTLLALAIQPKLRTFRNLLIA 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9 MWNSSDANFSCYHESVLGYRYVAVSWGVTGTVGNVLTLLALAIQPKLRTFRNLLIA 68

QY 61 NLTADLLCYTLQPFSDTYLHLHWRT 88
      |||||:|||||:|||||:|||||:|||||:|||||
Db 69 NLTADLLCYTLQPFSDTYLHLXWRT 96

RESULT 12
US-09-989-442-85
; Sequence 85, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ208
; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
```

; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/226,868
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/216,647
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/225,267
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/216,880
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/225,270
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/251,869
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/235,834
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/234,274
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: 60/234,223
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: 60/228,924
 ; PRIOR FILING DATE: 2000-08-30
 ; PRIOR APPLICATION NUMBER: 60/224,518
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/236,369
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/224,519
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/220,964
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 60/241,809
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/249,299
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/236,327
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/241,785
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/244,617
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: 60/225,268
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/236,368
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/251,856
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/251,868
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/229,344
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/234,997
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: 60/229,343
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,345
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,287
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,513
 ; PRIOR FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/231,413
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/229,509
 ; PRIOR FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/236,367
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/237,039
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/237,038
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/236,370
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/236,802
 ; PRIOR FILING DATE: 2000-10-02

; PRIOR APPLICATION NUMBER: 60/237,037
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/237,040
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/240,960
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/239,935
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: 60/239,937
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: 60/241,787
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/246,474
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: 60/246,532
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: 60/249,216
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,210
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/226,681
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/225,759
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/225,213
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/227,182
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/225,214
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/235,836
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/230,438
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/215,135
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: 60/225,266
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/249,218
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,208
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,213
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,212
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,207
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,245
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,244
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,217
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,211
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,215
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,264
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,214
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,297
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/232,400
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: 60/231,242
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/232,081
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/232,080
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/231,414

; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14

Query Match 22.2%; Score 454; DB 10; Length 116;
Best Local Similarity 98.9%; Pred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 60
Db 9 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 68

QY 61 NLTADLLCYCTLLQPFSDTYLHLHWRT 88
Db 69 NLTADLLCYCTLLQPFSDTYLHLHWRT 96

RESULT 13
US-09-764-886-60
; Sequence 60, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ02
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-886-60

Query Match 22.2%; Score 454; DB 10; Length 116;
Best Local Similarity 98.9%; Pred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 60
Db 9 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 68

QY 61 NLTADLLCYCTLLQPFSDTYLHLHWRT 88
Db 69 NLTADLLCYCTLLQPFSDTYLHLHWRT 96

RESULT 13
US-09-764-886-60
; Sequence 60, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ02
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-886-60

Query Match 22.2%; Score 454; DB 10; Length 116;
Best Local Similarity 98.9%; Pred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 60
Db 9 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 68

QY 61 NLTADLLCYCTLLQPFSDTYLHLHWRT 88
Db 69 NLTADLLCYCTLLQPFSDTYLHLHWRT 96

RESULT 13
US-09-764-886-60
; Sequence 60, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ02
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-886-60

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 60
Db 9 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 68

QY 61 NLTADLLCYCTLLQPFSDTYLHLHWRT 88
Db 69 NLTADLLCYCTLLQPFSDTYLHLHWRT 96

RESULT 14
US-09-764-875-641
; Sequence 641, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ02
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 641
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-875-641

Query Match 22.2%; Score 454; DB 11; Length 116;
Best Local Similarity 98.9%; Pred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 60
Db 9 MNSSDANFSCYHESVLGYRYVAVSWGVAVTGTGCVNLTLLALAIQPKLRTFRNLLIA 68

QY 61 NLTADLLCYCTLLQPFSDTYLHLHWRT 88
Db 69 NLTADLLCYCTLLQPFSDTYLHLHWRT 96

RESULT 15
US-09-764-886-60
; Sequence 60, Application US/09764886
; Publication No. US20020086822A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ02
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-886-60

; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-886-60

Query Match 22.2%; Score 454; DB 12; Length 116;
Best Local Similarity 98.9%; Pred. No. 1.5e-35;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MWNSSDANFSCYHESVLGYRYVAVSWGVVAVTGTGTVGNVLTLLALAIQPKLRTRENLLIA 60
Db 9 MWNSSDANFSCYHESVLGYRYVAVSWGVVAVTGTGTVGNVLTLLALAIQPKLRTRENLLIA 68

QY 61 NLTADLLYCTLLQPFSDTYLHLHWR 88
Db 69 NLTADLLYCTLLQPFSDTYLHLXWRT 96

Search completed: September 24, 2004, 08:57:02
Job time : 414 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 08:00:36 ; Search time 43 Seconds
(without alignments)
885.857 Million cell updates/sec

Title: US-10-029-436-2
Perfect score: 2041
Sequence: 1 MNSSDANFSCYHESVLYGR.....FRQAYGSILKGRPSFRLH 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	18.5	670	T13739	probable hormone r
2	309	15.1	572	T13740	probable hormone r
3	292.5	14.3	515	JC1525	alpha-1B-adrenergi
4	291	14.3	442	DYXLD2	dopamine receptor
5	290	14.2	443	DYHUD2	dopamine receptor
6	288.5	14.1	515	A40491	alpha-1-adrenergi
7	288	14.1	444	DYBOD2	dopamine receptor
8	286.5	14.0	517	A45121	alpha-1B adrenergi
9	286.5	14.0	592	T25837	hypothetical prote
10	283.5	13.9	444	DYMSD2	dopamine receptor
11	283.5	13.9	444	S08146	dopamine receptor
12	281.5	13.8	466	A35375	alpha-1-adrenergi
13	280	13.7	484	S58868	G protein-coupled
14	278.5	13.6	423	JC7677	allatostatin recep
15	278.5	13.6	466	I57959	alpha-1C adrenergi
16	274	13.4	429	S65656	alpha-1C-adrenergi
17	274	13.4	466	JN0765	alpha-1C-adrenergi
18	274	13.4	499	S65657	alpha-1C-adrenergi
19	272.5	13.4	400	G01977	d3 dopamine recept
20	272	13.3	477	S71323	alpha-1A adrenergi
21	270.5	13.3	511	C56849	dopamine receptor-
22	270.5	13.3	560	A38731	alpha-1A adrenergi
23	268.5	13.2	400	G00013	D3 dopamine recept
24	267.5	13.1	446	DYRTD3	dopamine receptor
25	267.5	13.1	446	I48322	dopamine receptor
26	266	13.0	400	S32804	beta-3-adrenergi
27	264.5	13.0	357	JC7319	probable allatosta
28	261.5	12.8	458	A40392	alpha-2-adrenergi
29	259	12.7	365	A45260	serotonin receptor

30	259	12.7	452	2	A46195	cholecystokinin B
31	257	12.6	400	2	A53281	beta 3-adrenergi
32	255	12.5	458	2	JS0616	serotonin receptor
33	255	12.5	514	2	D56849	dopamine receptor-
34	254.5	12.5	458	2	A48392	alpha 2C4 adrenoce
35	254.5	12.5	458	2	I49480	alpha-2 adrenergi
36	254	12.4	613	2	S70520	melatonin receptor
37	252.5	12.4	635	2	T37239	serotonin receptor
38	252.5	12.4	654	2	T29877	hypothetical prote
39	252.5	12.4	683	2	T37240	serotonin receptor
40	252	12.3	400	2	A41679	beta-3-adrenergi
41	251	12.3	394	2	JC7209	galanin receptor -
42	251	12.3	501	2	JH0447	alpha-1A-adrenergi
43	250	12.2	427	2	S50150	gastric CCK-A rece
44	250	12.2	572	2	I39369	alpha-1A-adrenergi
45	249	12.2	447	2	A47430	gastrin/cholecysto

ALIGNMENTS

RESULT 1

T13739
probable hormone receptor 22E5.11 [similarity] - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13739
R;Murphy, L.; Harris, D.; Barrell, B.
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17668
A;Accession: T13739
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-670 <MUR>
A;Cross-references: EMBL:AL031765; NID:e1371523; PID:e1326037; PIDN:CAA21123.1
C;Genetics:
A;Cross-references: FlyBase:FBgn0000667
A;Introns: 30/2; 77/2; 400/1
A;Note: EG:22E5.11

Query Match	18.5%;	Score 378;	DB 2;	Length 670;
Best Local Similarity	26.4%;	Pred. No. 2.5e-23;		
Matches	102;	Conservative	79;	Mismatches 165; Indels 40; Gaps 10;
Qy	7	ANFSCYHESVLGYRYVAVSVGWVAVTGTGVNVLTLALAIQPKLRTRNLLIANLT	AD	66
Db	26	ADATGFSQSLLTFAAVMT---FLIMIVGICGNLLTVVALLKCPKRVNVAFAFIISLCIAD	82	
Qy	67	LLYCTLLQPFVSVDYHLHWRTGATFCRVFGLLLFASNSVSILTLCLIALGRYLLIAHPK	126	
Db	83	LLFCALVLPFQGRFVQGTWRHGQVLCRLIPFIQYGNIGVSLLCIAMITINRYVMITHHG	142	
Qy	127	LFPQVFSAGIVLALVSTWVVGVSAPL-----WPIYILVPVVCIS-FDRIRGRPYTTI	181	
Db	143	LYARIYKRHWIAVMIAACWLFSGYGMQLPTLLGFWGRFGYDSRLQTCISIMTDDHGHSKTT	202	
Qy	182	LMGIYFVLGLSSVGIFYCLIHQRVAAQALDQYKLRQASIHNSNHVARTDEAMPGRFQEL	241	
Db	203	LFITAFVIPCLVIIACYAKIFWVVKSEQRKXKXKATKQNSI-----PNNLRPL	250	
Qy	242	DSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP-	300	
Db	251	AS-TGSGALPSGAECQP-----SNRVSSDSSSSFSIDVPETAP---SGKQOPT	294	
Qy	301	-IKGARRAPDSSEFGKVTMCFVFLCFALSYIPFLLNLILDARVQAPRVVHMLAANLT	359	
Db	295	RVKDQREVRKRNEW-RITKMVLAIFLSFVVCYLPITIVKVADKNVEHPS-LHICSYILL	352	
Qy	360	WLNCGINPVLAAAMNRQFQAYGSIL	385	
Db	353	YLSACINPIIYVIMNKQYKAYKTVV	378	

RESULT 2

Tl3740
probable hormone receptor 22E5.10 [similarity] - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: Tl3740
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17668
A;Accession: Tl3740
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-572 <MUR>
A;Cross-references: EMBL:AL031765; NID:el371523; PID:el329906; PIDN:CAA21124.1
C;Genetics:
A;Cross-references: FlyBase:FBgn0000667
A;Introns: 218/2; 426/2
A;Note: EG:22E5.10

Query Match 15.1%; Score 309; DB 2; Length 572;
Best Local Similarity 22.4%; Pred. No. 1.1e-17;
Matches 102; Conservative 83; Mismatches 180; Indels 90; Gaps 10;

QY 9 FSCYHESVLGYRYVAVSWGVAVTGTGNGVLTLLALAIQPKLRFNLLIANLTLDLL 68
Db 100 FEGYDELTLTIANVAC---IVFIIVGVPGNLLTIVALSRRGRQTRNSTAIFINLSCSDLL 156
QY 69 YCTLLQPFSDVTYHLHWRGATFCRVFGLLLFASNSVSLTCLIALGRYLLIAHPKLF 128
Db 157 FGCNPLPLAASFKEAWTHSDLLCLRFPLRLRYGLLAVSLLSVSLTINRYIIAHPQY 216
QY 129 PQVFSAGIVLALVSTVWVGVSFAP---LWPIYILVPVVTCTSPDRIR-GRPYTTILM 183
Db 217 PRIYQRYLALMVAGTWITTFSIMPTWRGVWGIFGLDVSIGSCSIMHMDRYGRSPKEFLF 276
QY 184 GIYFVLGLSSVGIFYCLYHQRVRAA-----QALDQYKLRQ 219
Db 277 IAAFMVPCICIVICVARIYIFLLVRKAIRAGTAGKTNVSDVTPSSAPQHQIQAMATPKKPE 336
QY 220 ASIHSNHVARTDAMPGRFQELDSRLASGSPSEISSEPV----- 260
Db 337 KVTSS--GEANEPIAGRPFFVVEENLAYIDDNASTDLSLPISYSIRRRDQDQPPVVDNV 394
QY 261 -----AATTQTLGDSSEVGDQINSKRAQMAEKSPPEA----- 294
Db 395 VLKEREKERDRQEKVSLGRSQTLKNGKTHGKNPITTSRITSFTRSPKSHYASMG 454
QY 295 SAKAQPIKAGARRAPDSSEFGKVTMCFVFLCFALSYPFLLNILDARVQAPRVH-- 352
Db 455 TSNASSIYPGR---MSAKDRRLKMLIVFVWFVICYLPITVAKIWSATE---VWTF 506
QY 353 -MLAANLTWLCINPVLVYAAANRQFQAYGSILK 386
Db 507 NIAGYLLIYLTTCINPLIYVLSSEYRAYWNLLR 541

RESULT 3

JC1525
alpha-1B-adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 13-Aug-1999
C;Accession: JC1525; S08400
R;Gao, B.; Kunos, G.
Gene 131, 243-247, 1993
A;Title: Isolation and characterization of the gene encoding the rat alpha 1B adrenergic
A;Reference number: JC1525; MUID:94010315; PMID:8406017
A;Accession: JC1525
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-515 <GAO>
A;Cross-references: GB:108610; NID:G202624; PIDN:AAA40647.1; PID:G202626

R;Voigt, M.M.; Kispert, J.; Chin, H.

Nucleic Acids Res. 18, 1053, 1990

A;Title: Sequence of a rat brain cDNA encoding an alpha-1B adrenergic receptor.

A;Reference number: S08400; MUID:90192094; PMID:2156222

A;Accession: S08400

A;Molecule type: mRNA

A;Residues: 1-202, 'C', 204-206, 'C', 208-305, 'C', 307-414, 'QK', 417-439, 'C', 441-483, 'ATA', 487-

A;Cross-references: EMBL:X51585; NID:G55557; PIDN:CAA35934.1; PID:G55558

C;Genetics:

A;Introns: 317/1

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 14.3%; Score 292.5; DB 2; Length 515;
Best Local Similarity 25.2%; Pred. No. 2.2e-16;
Matches 97; Conservative 71; Mismatches 150; Indels 67; Gaps 12;

QY 23 AVSWGVVVA---VTGTGNGVLTLLALAIQPKLRFNLLIANLTLDLLYCTLLQPFSD 79
Db 45 AISVGLVLGAFILFAIVGNILVSVACNRHLRTPTNYFIVNLATADLLSFTVLPSAT 104
QY 80 TYLHLHWRGATFCRVFGLLLFASNSVSLTCLIALGRYLLIAHPKLPQVFSAGIVL 139
Db 105 LEVLGVWVLRIFCDIWAADVLCCTASLSLCAISIDRYIGVYSLQYPTLVTRRKAIL 164
QY 140 ALVSTWVG-VASFPAL--WPIYILVPVVTCTSPDRIRGRPYTTILMGI-YFVLGLSSVG 195
Db 165 ALLSVWVLTSTVISIGPLLGWK---EPAPNDDKECGVTEEPFVALFSSLSGFIPLAVIL 220
QY 196 IFYCLIHQRVQKRAAQALDQYKLRQASISHNHVARTDEAMPGRFQELDSRLASGSPSEGIS 255
Db 221 VMYCRVYIVAKRTTKNLEAGVMKEMS-----NSKELTLRIHSKNFHE--- 262
QY 256 SEPVSAAATTQTLGDSSEVGDQINSKRAQMAEKSPPEASAKAQPIKGARRAPDSSEFG 315
Db 263 -----DTLSSTKAK---GHNPRSSIAVKLFKFSRE-KKAAKTLG 297
QY 316 KVTRMCFVFLCFALSYPFLL---LNILDARVQAPRVVHMLAANLTWLCINPVLVYAA 372
Db 298 IVVGM-----FILSWLPFFIALPLGSLFSTLKPDPDAVEKVVFWVWLFNSCLNPIIYPC 350
QY 373 MNQRFQAYGSILK---RGPRSPHR 394
Db 351 SSKEFKRAFVRLGQCRCRGRRRR 375

RESULT 4

DYXLD2
dopamine receptor D2 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: S14827
R;Martens, G.J.M.; Molhuizen, H.O.F.; Groeneveld, D.; Roubos, E.W.
FEBS Lett. 281, 85-89, 1991
A;Title: Cloning and sequence analysis of brain cDNA encoding a Xenopus D(2) dopamine rec
A;Reference number: S14827; MUID:91200321; PMID:1826663
A;Accession: S14827
A;Molecule type: mRNA
A;Residues: 1-442 <MAR>
A;Cross-references: EMBL:X59500; NID:G64648; PIDN:CAA42088.1; PID:G64649
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; neurotransmit
F;1-442/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F;1-232,266-442/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F;32-53/Domain: transmembrane #status predicted <TM1>
F;65-88/Domain: transmembrane #status predicted <TM2>
F;103-124/Domain: transmembrane #status predicted <TM3>
F;146-168/Domain: transmembrane #status predicted <TM4>
F;182-204/Domain: transmembrane #status predicted <TM5>
F;205-372/Domain: intracellular #status predicted <INT>
F;373-396/Domain: transmembrane #status predicted <TM6>
F;405-428/Domain: transmembrane #status predicted <TM7>
F;5,15,18,169/Binding site: carbohydrate (Asn) (covalent) #status predicted


```

F;223/Binding site: phosphate (Ser) (covalent) #status predicted
Query Match      14.3%; Score 291; DB 1; Length 442;
Best Local Similarity 24.6%; Pred. No. 2.4e-16;
Matches 111; Conservative 75; Mismatches 176; Indels 90; Gaps 13;

QY      8 NFSCYHESVLG-----YRYVAVSWGVAVTGTGVNLTLLALAIQPKLRPF 55
Db      5 NLSMYNDINNGTNGTAVDQKPHNYAYAMLLTLLVFI-VFGNVLVCIASVREKALQTT 63

QY      56 NLLIANLTADLLYCTLLQPFSDTYLHLHWRGTGATCRVFGLLLFASNSVSILTLCLIA 115
Db      64 NYLLIVSLAVADLLVATLVMPWAVYMEVVGWRFESRIHCDIFVLDVMMCTASILNLCAIS 123

QY      116 LGRYLLIAHPKLFPPQVFSAGKIVLALVSTWVVGVASFAPLWPIYILVPVC-----T 167
Db      124 IDRYTAVAMPMLYNTRYSSKRRVTVMIS--VVWLSEFA-----ISCPLLFGLNNTGSKV 175

QY      168 CSFDRIRGRPYTTIL-MGIYFVLGLSSVGIFYCLIHROVKRA-----AQALDQY---- 215
Db      176 CIIDNPAFVIYSSIVSFYVPFIVTLLVYVQIYIVLRKRRKRVNTKRNSRGVAVDAHKDKC 235

QY      216 -----KLRQASIHSHNHVARTDEAMPGRFQELDSRLASGGPSEGISSEPVSAATT----- 264
Db      236 THPEDVKLCVSVFKSNGSFPAKKKVLVQE-----AGKHPDEMEMEMSSSTSPPEKTK 289

QY      265 -QTLEGDSSEVGDIQNSKRAKQMAEKSPPEASAKAQ----- 299
Db      290 HKSASPDHNQLAVPATSNQCKNASLTSPVESPYKAENGHPKDSTKPAKVFEIQMPNGK 349

QY      300 ---PIKGARRAPDSSESSEFGKVTRMCFAVFLCFALSYIPFLLNLILDARVQAPRVVHMLAA 356
Db      350 TRTSIKTMSKKKLSQHEKKATQMLAIVLGVFIIICWLPPFFIIHLNMHCNC-NIPQALYS 408

QY      357 NLTWL---NGCINPVLVYAAMNRQFQAYGSIL 385
Db      409 AFTWLGVYNSAVNPIIYTTTFNVEFRKAFIKIL 440

```

RESULT 5
DYHUD2
dopamine receptor D2 - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 21-Jul-2000
C:Accession: S08417; S09618; S20842; A33392; A34502; A37013; A37384; A48409; S40694
C:Robakis, N.K.; Mohamadi, M.; Fu, D.Y.; Sambamurti, K.; Refolo, L.M.
Nucleic Acids Res. 18, 1299, 1990
A:Title: Human retina D2 receptor cDNAs have multiple polyadenylation sites and differ f
A:Reference number: S08417; MUID:90206805; PMID:2138729
A:Accession: S08417
A:Molecule type: mRNA
A:Residues: 1-443 <ROB>
A:Cross-references: EMBL:X51362; NID:G30495; PIDN:CAA35746.1; PID:G30496
R:Jalal Toso, R.; Sommer, B.; Ewert, M.; Herb, A.; Pritchett, D.B.; Bach, A.; Shivers, B.D
EMBO J. 8, 4025-4034, 1989
A:Title: The dopamine D2 receptor: two molecular forms generated by alternative splicing
A:Reference number: S09618; MUID:90076122; PMID:2531656
A:Accession: S09618
A:Molecule type: mRNA
A:Residues: 1-443 <DAL>
A:Cross-references: EMBL:X51645; NID:G30867; PIDN:CAB56463.1; PID:G5921480
A:Accession: S20842
A:Molecule type: DNA
A:Residues: 179-379 <DA2>
A:Cross-references: EMBL:X51646; NID:G30868; PIDN:CAB37869.1; PID:G4467834
R:Selbie, L.A.; Hayes, G.; Shine, J.
DNA 8, 683-689, 1989
A:Title: The major dopamine D2 receptor: molecular analysis of the human D2-A subtype.
A:Reference number: A33392; MUID:90126238; PMID:2533064
A:Accession: A33392
A:Molecule type: mRNA
A:Residues: 1-443 <SEL>
A:Cross-references: GB:M30625; NID:q181431; PIDN:AAA88024.1; PID:q181432

R;Grandy, D.K.; Marchionni, M.A.; Makam, H.; Stofko, R.E.; Alfano, M.; Frothingham, L.;
Proc. Natl. Acad. Sci. U.S.A. 86, 9762-9766, 1989
A;Title: Cloning of the cDNA and gene for a human D-2 dopamine receptor.
A;Reference number: A34502; MUID:9009344; PMID:2532362
A;Accession: A34502
A;Molecule type: mRNA
A;Residues: 1-443 <STO>
A;Cross-references: GB:M29066; NID:G181828; PIDN:AAA52761.1; PID:G181829; GB:M77247; GB:M
R;Stormann, T.M.; Gdula, D.C.; Weiner, D.M.; Brann, M.R.
Mol. Pharmacol. 37, 1-6, 1990
A;Title: Molecular cloning and expression of a dopamine D2 receptor from human retina.
A;Reference number: A37013; MUID:90136534; PMID:2137193
A;Accession: A37013
A;Molecule type: mRNA
A;Residues: 1-241,271-443 <STO>
R;Selbie, L.A.; Hayes, G.; Shine, J.
Adv. Second Messenger Phosphoprotein Res. 24, 9-14, 1990
A;Title: DNA homology screening: isolation and characterization of the human D2-A dopamine
A;Reference number: A37384; MUID:91000955; PMID:2144985
A;Accession: A37384
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-443 <SE2>
A;Experimental source: fetal brain and pituitary
R;Deary, A.; Falardeau, P.; Shores, C.; Caron, M.G.
Cell. Mol. Neurobiol. 11, 437-453, 1991
A;Title: D2 dopamine receptors in the human retina: cloning of cDNA and localization of r
A;Reference number: A48409; MUID:92076439; PMID:1835903
A;Accession: A48409
A;Molecule type: mRNA
A;Residues: 1-241,271-443 <DEA>
A;Cross-references: GB:S69899; NID:G240290; PIDN:AAB20571.1; PID:G240291
A;Experimental source: retina
A;Note: sequence extracted from NCBI backbone (NCBIN:69899, NCBIP:69900)
R;Araki, K.; Kuwano, R.; Morii, K.; Hayashi, S.; Minoshima, S.; Shimizu, N.; Katagiri, T
Neurochem. Int. 21, 91-98, 1992
A;Title: Structure and expression of human and rat D2 dopamine receptor genes.
A;Reference number: S40694; MUID:93264902; PMID:1363862
A;Accession: S40694
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-39,'R',41-443 <ARA>
A;Cross-references: GB:S62137; NID:G405309; PIDN:AAB26819.1; PID:G405310
C;Genetics:
A;Gene: GDB:DRD2
A;Cross-references: GDB:119852; OMIM:126450
A;Map position: 11q23.1-11q23.1
A;Introns: 178/1, 241/3, 270/3, 380/1
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
F;1-443/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F;1-241,271-443/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F;38-59/Domain: transmembrane #status predicted <TM1>
F;71-94/Domain: transmembrane #status predicted <TM2>
F;109-130/Domain: transmembrane #status predicted <TM3>
F;152-174/Domain: transmembrane #status predicted <TM4>
F;188-210/Domain: transmembrane #status predicted <TM5>
F;211-373/Domain: intracellular #status predicted <CYT>
F;374-397/Domain: transmembrane #status predicted <TM6>
F;406-429/Domain: transmembrane #status predicted <TM7>
F;5,17,23/Binding site: carboxylate (Asn) (covalent) #status predicted
F;107-182/Disulfide bonds: palmitate (Cys) (covalent) #status predicted
F;443/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 14.2%; Score 290; DB 1; Length 443;
Best Local Similarity 25.8%; Pred. No. 3e-16;
Matches 114: Conservative 65; Mismatches 183; Indels 80; Gaps 15;

OV 62 LTLADLLYCTLLQPFSVDTYLHL--HWRTGATFCRVFGLLLFASNSVSILTCLIALGRY 119

```

Db      76 LAVADLLVATLVMPWV--YLEVVGWKEKFSRIHCDIFVTLDVMMCTASILNLCAISIDRY 133
QY      120 LLIAPKLPQVESAKGIVLALVSTVWVGFAPLWPIYILVVPVCTCSFDRIRGRPYT 179
Db      134 TAVAMPMLYNTRYSSKRRVTVMIS--IVVLSFT-----ISCPLLFGLNNADQNE 181
QY      180 TILMGIYFVLGLSSVGIF-----YCLIHQ-----VKRAAQAL----- 212
Db      182 CIIANPAFVVYSSIVSYFVPIVITLLVYIKIYIVLRRRRKRVTNKRSSRAFRHLRAPLK 241
QY      213 -----DQYKLRQASIHNSN---HVAETDEAMPGRFQELD-SRLASGPGSEGISSEPVSA 262
Db      242 GNCNTHPEDMKLCTVIMKSNGLFPVRRRRVVEAARRAQAELEMELSTSPPTRYSPIPPS 301
QY      263 TTQTLGDSSEVG-----DQINSKRAKQMAEKSPPEASAKAQPIKGARR 306
Db      302 HHQLTLPDPSHGLHSTPDSAPKPEKNGHAKDHPKIAKIFEIQTMPNGKTRTS-LKTMSR 360
QY      307 APDSSEFGKVTMCFEAVFLCFALSYPFLLNILDARVQAPRVVHMLAANLTWL---NG 363
Db      361 RKLQQKEKKATQMLAIVLGVFIICWLPFFITHILNIHCDN-NIPPVLYSAFTWLGYNVS 419
QY      364 CINPVLYAAMNRQFRQAYGSIL 385
Db      420 AVNPPIYTTFNIEFRKAFKIL 441

RESULT 6
A40491
alpha-1-adrenergic receptor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C;Accession: A40491
R;Cotecchia, S.; Schwinn, D.A.; Randall, R.R.; Lefkowitz, R.J.; Caron, M.G.; Kobilka, B.
Proc. Natl. Acad. Sci. U.S.A. 85, 7159-7163, 1988
A;Title: Molecular cloning and expression of the cDNA for the hamster alpha-1-adrenergic
A;Reference number: A40491; MUID:89017157; PMID:2845398
A;Accession: A40491
A;Molecule type: mRNA
A;Residues: 1-515 <COT>
A;Cross-references: GB:J04084; NID:G619407; PIDN:AAA58964.1; PID:G619408
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match      14.1%; Score 288.5; DB 2; Length 515;
Best Local Similarity 25.1%; Pred. No. 4.7e-16;
Matches 103; Conservative 74; Mismatches 162; Indels 71; Gaps 14;

QY      2 WNS-SDANFSCYHE-----SVLGYYV--AVSWGUVVA---VTGTGVNLTLLALAIQPKL 51
Db      17 WGEKLOANFTGENQTSNSTLPQLDVTTRAISGLVLGAPILFAIVGNILVILSVACNRHL 76
QY      52 RTRFNLLIANLTADLLYCTLLQPFSSVDTYLHLHWRGTGATFCRVFGLLLFASNSVSIITL 111
Db      77 RTPTNYFIVNLAADLLLSFTVLPFSATLEVLGYVWLGRIFCDIWAADVLCCTASILSL 136
QY      112 CLIALGRYLLIAHPKLPQVFSAGKIVLALVSTWVG-VASFAPL--WPIYILVPVVTCTC 168
Db      137 CAISIDRYIGVYSYLSQYPTLVTRRKAILALLSVWLSTVISIGPLLGWK----EPAPND 192
QY      169 SFDRIRGRPYTILMGI-YFVLGLSSVGIFYCLIHQVQKRAQALDQYKLRQASIHNSHV 227
Db      193 KECGVTEEPFYALPSSLSGSFYIPLAVILVMYCRVIVAKRTTKNLEAGVMKEMS----- 246
QY      228 ARTDEAMPGRFQELDSRLASGPGSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMA 287
Db      247 -----NSKELTLRIHSKNFHE-----DTLSSTKAK--- 271
QY      288 EKSPPEASAKAQPIKGARRAPDSSSEFGKVTMCFEAVFLCFALSIVIPFLL---LNILDAR 344
Db      272 -GHNPRSSIAVKLFKFSRE-KKAAKTLGIVVGM-----FILCWLPFFIALPLGSLFST 322

```

```

QY      345 VQAPRVVHMLAANLTWNGCINPVLYAAMNRQFRQAYGSILKRGPRSFHR 394
Db      323 LKPPDAVFKVFWLGYENSCLNPIIYPCSKKEFKRAFMRIILGCQCKSGRR 372

RESULT 7
DYBOD2
dopamine receptor D2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: S08163
R;Chio, C.L.; Hess, G.F.; Graham, R.S.; Huff, R.M.
Nature 343, 266-269, 1990
A;Title: A second molecular form of D2 dopamine receptor in rat and bovine caudate nuclei
A;Reference number: S08163; MUID:90136899; PMID:2137198
A;Accession: S08163
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-444 <CHI>
A;Cross-references: GB:X51657; NID:G304; PIDN:CAA35970.1; PID:G305
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
F;1-444/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F;1-241,271-444/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F;39-59/Domain: transmembrane #status predicted <TM1>
F;71-94/Domain: transmembrane #status predicted <TM2>
F;109-130/Domain: transmembrane #status predicted <TM3>
F;152-174/Domain: transmembrane #status predicted <TM4>
F;188-210/Domain: transmembrane #status predicted <TM5>
F;211-374/Domain: intracellular #status predicted <CYT>
F;375-398/Domain: transmembrane #status predicted <TM6>
F;407-430/Domain: transmembrane #status predicted <TM7>
F;5,17,23/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;107-182/Disulfide bonds: #status predicted
F;444/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match      14.1%; Score 288; DB 1; Length 444;
Best Local Similarity 26.8%; Pred. No. 4.4e-16;
Matches 112; Conservative 65; Mismatches 181; Indels 60; Gaps 14;

QY      19 YRYVAVSWGIVVAVTGTGVNLTLLALAIQPKLRTFRNLLIANLTADLLYCTLLQPFVS 78
Db      34 YNYAYAMLLTLLIFVI-VFGNVLVCMVAVSREKALQTTTNYLIVSLAVADLLVATLVMPWV 92
QY      79 DTYLHL--HWRTGATFCRVFGLLLFASNSVSIITLCLIALGRYLLIAHPKLPQVFSAGK 136
Db      93 --YLEVVGWKEKFSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKR 150
QY      137 IVLALVSTWVVGVSFAPLWPIYILVVPVCTCSFDRIRGRPYTILMGI-----YFVLG 190
Db      151 RVTVMIA--IVVLSFTISCP--MLFGLNNTDQNECIANPAFVYSSIVSYFVPFIVTL 206
QY      191 LSSVGIFYCLIHQ---VKRAAQAL-----DQYKLRQASIHNSN---HVA 228
Db      207 LVYIKIYIVLRRRKRVNTRKSSRAFRANLKAPLKGNCTHPEDMKLCTVIMKSNGLSPVN 266
QY      229 RTDEAMPGRFQELD-SRLASGPGSEGISSEPVSAATTQTLEGDSSEVG----- 275
Db      267 RRRVEAARRAQAELEMELSTSPPTRYSPIPPSHHQLTLPDPSHHGLHSTPDSPAKPE 326
QY      276 -----DQINSKRAKQMAEKSPPEASAKAQPIKGARRAPDSSSEFGKVTMCFEAVFLCFAL 330
Db      327 KNGHAKTVNPKIAKIFEIQSMFNGKTRTS-LKTMSSRRKLSQKKEKATQMLAIVLGVFII 385
QY      331 SYIPFLLNILDARVQAPRVVHMLAANLTWL---NGCINPVLYAAMNRQFRQAYGSIL 385
Db      386 CWLPFFITHILNIHCDN-NIPPVLYSAFTWLGYNVSAVNPIYTTFNIEFRKAFKIL 442

RESULT 8
A45121
alpha-1B adrenergic receptor - human
C;Species: Homo sapiens (man)

```

C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Apr-2000
C;Accession: A45121; JC2332
R;Ramara, C.S.; Denker, J.M.; Perez, D.M.; Gaivin, R.J.; Riek, R.P.; Graham, R.M.
J. Biol. Chem. 267, 21936-21945, 1992
A;Title: Genomic organization and expression of the human alpha 1B-adrenergic receptor.
A;Reference number: A45121; MUID:93016158; PMID:1328250
A;Accession: A45121
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-517 <RAM>
A;Cross-references: GB:M99590; NID:g178211
A;Note: sequence extracted from NCBI backbone (NCBIP:116785)
A;Note: this translation is not annotated in GenBank entry HUMADRENB, release 113.0 #dat
R;Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.;
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A;Title: Cloning, expression and characterization of human alpha adrenergic receptors al
A;Reference number: JC2331; MUID:94296402; PMID:8024574
A;Accession: JC2332
A;Molecule type: mRNA
A;Residues: 1-158, 'P', 160-244, 'H', 246-314, 'F', 316-380, 382-517 <WEI>
C;Genetics:
A;Gene: GDB:ADRA1B
A;Cross-references: GDB:127901; OMIM:104220
A;Map position: 5q31.1-5q33.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;39-72/Domain: transmembrane #status predicted <TM1>
F;81-111/Domain: transmembrane #status predicted <TM2>
F;121-146/Domain: transmembrane #status predicted <TM3>
F;157-184/Domain: transmembrane #status predicted <TM4>
F;203-227/Domain: transmembrane #status predicted <TM5>
F;290-320/Domain: transmembrane #status predicted <TM6>
F;326-360/Domain: transmembrane #status predicted <TM7>

Query Match 14.0%; Score 286.5; DB 2; Length 517;
Best Local Similarity 24.9%; Pred. No. 7e-16;
Matches 96; Conservative 71; Mismatches 151; Indels 67; Gaps 12;

QY 23 AVSWGVA--VTCFVGNVLTLLALAIQPKLRFNLLIANLTADLLYCTLLQPFSD 79
DB 45 AISVGLVGAFLFAIVGNILVILSVACNRHLRFTPTNYFIVNLAMADLLSFTVLPFSA 104
QY 80 TYLHLHWRGTATCFRVEGLLLFASNSVSIITLCLIALGRYLLIAHPKLPQVFSAGIVL 139
DB 105 LEVLGYVWLGRIFCDIWAADVLCCTASILSLCAISIDRYIGVRYSLQYPTLVTRRKAIL 164
QY 140 ALVSTWVVG-VASFAPL--WPIYILVPVVTCTCFDRIRGRPYTTILMGI-YFVLGLSSVG 195
DB 165 ALLSVVVLSTVISIGPLLGWK---EPAPNDDKECGVTEEPFYALFSSLSGYIPLAVIL 220
QY 196 IFYCLIHROVKRAAQALDOYKLRQASIHNSNHVARTDEAMPGRFQELDSRLASGGPSEGIS 255
DB 221 VMYCRVYIVAKRTTKNLEAGVMKEMS-----NSKELTLRIHKNFHE--- 262
QY 256 SEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPEASAKAQPIKGARRAPDSSEFG 315
DB 263 -----DTLSSTKAK---GHNPRSSIAVKLFKFSRE-KKAAKTLG 297
QY 316 KVTRMCPAVFLCFALSYTFLL--LNILDARVQAPRVVHMLAANLTWLNCGINPVLAA 372
DB 298 IVVGM-----FILCWLEFFIALPLGSLFSTLKPDAVKVFWLGYFNSCLNPIIYPC 350
QY 373 MNRQFRQAYGSILK---RGRSFHR 394
DB 351 SSKEFKRAVFRILGCQCRGRRRRR 375

RESULT 9
T25837
hypothetical protein M03F4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T25837

F;71-94/Domain: transmembrane #status predicted <TM2>
F;109-130/Domain: transmembrane #status predicted <TM3>
F;152-174/Domain: transmembrane #status predicted <TM4>
F;188-210/Domain: transmembrane #status predicted <TM5>
F;211-374/Domain: intracellular #status predicted <INT>
F;375-398/Domain: transmembrane #status predicted <TM6>
F;407-430/Domain: transmembrane #status predicted <TM7>
F;5,17,23/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;107-182/Disulfide bonds: #status predicted
F;228,229/Binding site: phosphate (Ser) (covalent) #status predicted
F;444/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 13.9%; Score 283.5; DB 1; Length 444;
Best Local Similarity 25.6%; Pred. No. 1e-15;
Matches 112; Conservative 70; Mismatches 185; Indels 71; Gaps 16;

QY 2 WNSDANFSCYHESVLGYRYVAVSWGVVAVTGTGVNLTLLALAIQPKLRTRFNLLIAN 61
Db 22 FNGSEGKADRPH-----YNYIAMLLTLIFII-VFNGNVLVCMVAVSREKALQTTNYLIVS 75

QY 62 LTLADLLYCTLLQPFVSDTYLHL--HWRTGATFCRVFGLLLFASNVSILTCLIALGRY 119
Db 76 LAVADLLVATLVMPWV--YLEVVGWKEKFSRIHCDIFVTLDVMMCTASILNLCAISIDRY 133

QY 120 LLIAHPKLPQVFSAGKIVLALVS-TWVGVASFAPLWPIYILVPVCTCSFDRIRGRPY 178
Db 134 TAVAMPMLYNTRYSSKRRVTVMIAVWLSFTISCPL-----LFGLNNTDQNECIANPA 188

QY 179 TTILMGI-----YFVLGLSSVGIFYCLIHQRQ-----VKRAAQAL-----D 213
Db 189 FVYSSIVSFYVPFIVTLVYIKIYIVLKRKRKRVNTKSSRAFRANLKTPLKGNCTHPE 248

QY 214 QYKLRQASIHNSN-----HVARTEAMPGRFOELD-SRLASGGPSEGISSEPVSAATTQTL 267
Db 249 DMKLCVTIMKSNNGSFVNNRRRMDAAR--RAQELEMEMLSSTSPPERTRYSPIPPSSHQLT 306

QY 268 EGDSEVSG-----DQINSKRAKQMAEKSPPEASAKAQPIKGARRAPDS 310
Db 307 LPDPGHHGLHNSPDSPAKPEKXGHAKIVNPRIAKFFEIQTMPNGKTRTS-LKTMGRRLS 365

QY 311 SSEFGKVTRMCFVFLCFALSYIPFLLNLNILDARVQAPRVVHMLAANLTWL---NCCINP 367
Db 366 QQKEKATQMLAIVLGVFIICWLPFFIITHILNIHDCD-NIPPVLYSAFTWLGYNVNSAVNP 424

QY 368 VLYAAMNRQFRQAYGSIL 385
Db 425 IITYTTNIEFRKAEMKIL 442

RESULT 12
A35375
alpha-1-adrenergic receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C;Accession: A35375
R;Schwinn, D.A.; Lomasney, J.W.; Lorenz, W.; Szklut, P.J.; Freneau Jr., R.T.; Yang-Feng, J. Biol. Chem. 265, 8183-8189, 1990
A;Title: Molecular cloning and expression of the cDNA for a novel alpha-1-adrenergic rec
A;Reference number: A35375; MUID:90243698; PMID:1970822
A;Accession: A35375
A;Molecule type: mRNA
A;Residues: 1-466 <SCH>
A;Cross-references: GB:J05426; NID:g162663; PIDN:AAA30374.1; PID:g162664
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

Query Match 13.8%; Score 281.5; DB 2; Length 466;
Best Local Similarity 23.0%; Pred. No. 1.6e-15;
Matches 95; Conservative 82; Mismatches 153; Indels 83; Gaps 13;

QY 3 NSSDANFSCYHESVLGYRYVAVSWGVTVA---VTGTGVNLTLLALAIQPKLRTRFNLLI 59
Db 7 NASDSS-NCTHPPPPVNISKAILGLGVLGILFVGLNVLVLSVACHRLHLSVTHYVI 65

QY 60 ANTLADLLYCTLLQPFVSDTYLHLHWRTGATFCRVFGLLLFASNVSILTCLIALGRY 119
Db 66 VNLAADLLLTSTVLPFSAIFEILGYWAFGRVFCNVWAAVDVLCCTASIMGLCIISIDRY 125

QY 120 LLIAHPKLPQVFSAGKIVLALVSTWVVG-VASFAPLWPIYILVP---VVCTCSFDRIRG 175
Db 126 IGVSYPLEPYTIVTQKRGMLALCVWALSLSVISIGPLFGWRQPAPADETIC-----QINE 180

QY 176 RPYTTILMGI-YFVLGLSSVGIFYCLIHQRVQKRAAQALDQYKLRQASIHNSHVARTDEAM 234
Db 181 EPGYVLFSAIGSFYVPLTIIILVMYCRVYVAVAKRESRGL----- 218

QY 235 PGRFQELDSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDIQINSKRAKQMAEKSPPEA 294
Db 219 -----KSGLKTD-----KSDSEQVTLRIHRKNA-QVGGSGVTSA 251

QY 295 SAK-----AQPIKGARRAPDSSESSEFGKVTRMCFVFLCFALSYPFLLLNILDA---RVQA 347
Db 252 KNTHTFSVRLKFSREK-----KAAKTGLIVVGCFLVCLWLPFFFLVMPIGSFFPDRP 303

QY 348 PRVHMLAANLTWLNKCINPVLYAAMNRQFRQAYGSI-----LKRGRPSFHRL 395
Db 304 SETVFKIAFWLGYLNSCINPIIYPCSSQEFKKAQFQNVLRIOCLRRKQSSKHTL 356

RESULT 13
S58868
G protein-coupled receptor GCR1 - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 17-Nov-2000
C;Accession: S58868; S58869
R;Vanden Broeck, J.; Vultsteke, V.; Huybrechts, R.; De Loof, A. J. Neurochem. 64, 2387-2395, 1995
A;Title: Characterization of a cloned locust tyramine receptor cDNA by functional expres
A;Reference number: S58868; MUID:95279966; PMID:7760020
A;Accession: S58868
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-484 <VAN>
A;Cross-references: EMBL:X69520; NID:g871404; PIDN:CAA49268.1; PID:g871405
A;Accession: S58869
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-307,'D',309-338,'K',340-484 <VA2>
A;Cross-references: EMBL:X69521; NID:g871406; PIDN:CAA49269.1; PID:g871407
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992
C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor

Query Match 13.7%; Score 280; DB 2; Length 484;
Best Local Similarity 24.5%; Pred. No. 2.2e-15;
Matches 111; Conservative 63; Mismatches 187; Indels 92; Gaps 17;

QY 15 SVLGYRYVAVSWGVVAVTG-----TVGNVLTLLALAIQPKLRTRFNLLIANLTAD 66
Db 38 SVLGVRLAVPEWEVAVTAVSLSLIILITIVGNVLVLSVFTYKPLRIVQNFFIVSLAVAD 97

QY 67 LLYCTLLQPFVSDTYLHLHWRTGATFCRVFGLLLFASNVSILTCLIALGRYLLIAHPK 126
Db 98 LTVAVLMPFNVAYSLSIQRVVFGIVVCKMWLTCDVLCCTASILNLCAALDRYWAITDPI 157

QY 127 LFPQVFSAGKIVLALVSTWVV-GVASFAPL-----WPIYI--LVPVVTCSFDRIRGRPY 178
Db 158 NYAQKRTLRRVLAMTAGVWLLSGVISSPPLIGMNDWPMFNDTTP-----COLTEEQGYVI 213

QY 179 TTILMGIY---FVLGLSSVGIFYCLIHQRVKRAA-----QALDQYKLRQA----- 220
Db 214 YSSLGSFFIPLFIMTIVYVEIFATKRRRLREKAKSKLNSAMKQQAQAVPSSVPSHDQ 273

QY 221 ---SIHNSH-----VARTDEAMPGRF-----QELDSRLAS 247
Db 274 ESVSSETNHNELPPPPAPPSKEKRRKTKKSKKKEAAEGRFLAPAMVAEDSVTDNSVS 333

QY 248 GGP--SEGISEPVSAAATTTTLEGDSSEVDQINSKRAKQMAEKSP--EASAKAQP----- 300
 Db 334 VGPVARNHLAEDGYCTTTTTTTTTTAUTDSRSTASQSGSTAPPTVPQKSIPIVYQF 393
 QY 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYIPFLLLNIL-----DARVOAPRVVHMLA 355
 Db 394 IEEKQRI--SLSKERRAARTLGIIMGVGVVWVWLPFFFLMYVIVPFCNPCKSPKLVNF-- 449
 QY 356 ANLTWL--NGCINPVLVYAMNRQFRQAYGSIL 385
 Db 450 --ITWLGYNINSALNPIIYTIENLDFRRAFKLL 480

RESULT 14
 JC7677
 allatostatn receptor - American cockroach
 C;Species: Periplaneta americana (American cockroach)
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
 C;Accession: JC7677
 R;Auerwald, L.; Birguet, N.; Gaede, G.; Kreienkamp, H.J.; Richter, D.
 Biochem. Biophys. Res. Commun. 282, 904-909, 2001
 A;Title: Structural, functional, and evolutionary characterization of novel members of
 A;Reference number: JC7677; MUID:21250673; PMID:11352636
 A;Accession: JC7677
 A;Molecule type: mRNA
 A;Residues: 1-423 <AUE>
 A;Cross-references: GB:AF336364
 C;Comment: This receptor, for the neuropeptide, is involved in the inhibition of juveni
 C;Genetics:
 A;Gene: Alstr
 C;Keywords: neuropeptide; transmembrane protein
 F;73-94/Domain: transmembrane #status predicted <TM1>
 F;105-127/Domain: transmembrane #status predicted <TM2>
 F;143-164/Domain: transmembrane #status predicted <TM3>
 F;165-167/Region: active element DRF
 F;187-207/Domain: transmembrane #status predicted <TM4>
 F;243-264/Domain: transmembrane #status predicted <TM5>
 F;290-312/Domain: transmembrane #status predicted <TM6>
 F;327-350/Domain: transmembrane #status predicted <TM7>

Query Match 13.6%; Score 278.5; DB 2; Length 423;
 Best Local Similarity 23.1%; Pred. No. 2.5e-15;
 Matches 94; Conservative 64; Mismatches 116; Indels 133; Gaps 13;
 QY 22 VAVSWGVAVTGTGTVGNVLTLLALAIQPKLRTRENLNLTADLLYCTLLQPFSDTY 81
 Db 71 VPLLFGLLV-LGFGNALVVLVVAANQMRSTTNLLINLAVADLLFVFCVPTATDY 129
 QY 82 LHLHRTGATCFRVFGLLLFASNSVILTCLIALGRVLLIAHPKLPQVFSAGVIAL 141
 Db 130 VLPFPFGDIWKIVQYLIIVTVAYASVYTLVMSLDRFLAVVHPITMSIRTERNAIAI 189
 QY 142 VSTWVGVASFAPLWPIYILVPV-----CTCSF---DRIRGRP-----YTILMGI 185
 Db 190 AVTWVILLASVPVYLSHGEVTVYSSAHTACVFLPADPI-NRPDGYNKPVQIIFAT 248
 QY 186 YFVLGLSSV-GIFYCLIHROVXRAAALDQYKLRQASIHSHVARTDEAMPGRFQELDSR 244
 Db 249 SYVTPLALICGLYLWLLVRLMGAA-----SRRGK----- 273
 QY 245 LASGSPSEGISSEPVSAATTTLEGDSSEVDQINSKRAKQMAEKSPPEASAKAPIKA 304
 Db 274 -----PGHVSAE-----SRRGK----- 287
 QY 305 RRAPDSSEFGKVTMCFVFLCFALSYIPFLLLNIL-----DARVOAPRVVHMLA 355
 Db 288 -----RVTRMVVVVVAIFAVCVFPIQLILVLSKVDKYEITNTSVMIQIVSHVLA 336
 QY 356 ANLTWLGNCINPVLVYAMNRQFRQAYGSIL-----KRGPRSFHR 394
 Db 337 -----YMNVCVNPILYAFLSHDFRKAFRKVINCGSAQRAQPGPR-YHR 378

RESULT 15
 I57959
 alpha-1C adrenergic receptor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Apr-2000
 C;Accession: I57959; I52862; PC2179
 R;Laz, T.M.; Forray, C.; Smith, K.E.; Bard, J.A.; Vaysse, P.J.; Branchek, T.A.; Weinshank
 Mol. Pharmacol. 46, 414-422, 1994
 A;Title: The rat homologue of the bovine alpha 1C-adrenergic receptor shows the pharmaco
 A;Reference number: I57959; MUID:95021119; PMID:7935320
 A;Accession: I57959
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-466 <RES>
 A;Cross-references: EMBL:U07126; NID:G595275; PIDN:AAA62866.1; PID:G595276
 R;Stewart, A.F.; Rokosh, D.G.; Bailey, B.A.; Karns, L.R.; Chang, K.C.; Long, C.S.; Kariya
 Circ. Res. 75, 796-802, 1994
 A;Title: Cloning of the rat alpha 1C-adrenergic receptor from cardiac myocytes. alpha 1C
 A;Reference number: I52862; MUID:95008062; PMID:7923624
 A;Accession: I52862
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-38, 'L', 40-66, 'G', 68-466 <RE2>
 A;Cross-references: EMBL:U13368; NID:G555851; PIDN:AAA52103.1; PID:G555852
 R;Rokosh, D.G.; Bailey, B.A.; Stewart, A.F.R.; Karns, L.R.; Long, C.S.; Simpson, P.C.
 Biochem. Biophys. Res. Commun. 200, 1177-1184, 1994
 A;Title: Distribution of alpha 1C-adrenergic receptor mRNA in adult rat tissues by RNase
 A;Reference number: PC2179; MUID:94241969; PMID:8185565
 A;Accession: PC2179
 A;Molecule type: mRNA
 A;Residues: 102-279 <ROK>
 A;Experimental source: cardiac myocyte
 C;Comment: This factor comprises a multigene family. As do alpha-2 and beta-adrenergic r
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: neurotransmitter receptor; transmembrane protein
 F;26-42/Domain: transmembrane #status predicted <TM1>
 F;73-89/Domain: transmembrane #status predicted <TM2>
 F;104-120/Domain: transmembrane #status predicted <TM3>
 F;147-163/Domain: transmembrane #status predicted <TM4>
 F;195-211/Domain: transmembrane #status predicted <TM5>
 F;276-292/Domain: transmembrane #status predicted <TM6>
 F;306-329/Domain: transmembrane #status predicted <TM7>

Query Match 13.6%; Score 278.5; DB 2; Length 466;
 Best Local Similarity 23.1%; Pred. No. 2.8e-15;
 Matches 97; Conservative 78; Mismatches 148; Indels 97; Gaps 14;
 QY 3 NSSDANFSCYHESVLGYRYVAVSWGVA---VTGTGTVGNVLTLLALAIQPKLRTRENLII 59
 Db 7 NASEGS-NCTHPPAPVNIKAILLGVILGGLIIFGVLGNILVILSVACHRHLSVTHYII 65
 QY 60 ANLTADLLYCTLLQPFSDTYLHLHRTGATFCRVFGLLLFASNSVILTCLIALGRY 119
 Db 66 VNLAVADLLLTSTVLPFSAIFELGYWAFGRVFCNTWAAVDVLCCTASIMGLCLISIDRY 125
 QY 120 LLIAHPKLPQVFSAGKIVLALVSTWVVG-VASFAPLWPIYILVP---VVTCTSFDRIRG 175
 Db 126 IGVSYPLRYPTIVTQRRGVRAALLCVWVLSLVISIGLFGWRQPAPEDETIC-----QINE 180
 QY 176 RPYTTILMGI-YFVLGLSSVGIIFYCLIHROVXRAAAL-----DQYKLRQASIH 223
 Db 181 EPGYVLFSAIGSFYVPLAILVMYCRVYVAVKRESRGLKSLKTDKSDSEQVTLR---IH 237
 QY 224 SNHVARTDEAMPGRFQELDSRLASGGPSEGISSEPVSAATTTLEGDSSEVDQINSKRA 283
 Db 238 RKNV-----PAEG---GGVSSAKNKT-----HFSVRL 262
 QY 284 KQMAEKSPPEASAKAPIKARRAPDSSESSEFGKVTMCFVFLCFALSYIPFLLLNILDA 343
 Db 263 KFSREK-----KAAKTGLIWGCVLWLPFLVMPIGS 296
 QY 344 ---RVQAPRVVHMLAANLTWLGNCINPVLVYAMNRQFRQAYGSI-----LKRGRSFHRL 395

Db 297 FFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNVLRIOCLRRRQSSKHAL 356

Search completed: September 24, 2004, 08:40:17
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 04:51:55 ; Search time 24 Seconds
(without alignments)
859.158 Million cell updates/sec

Title: US-10-029-436-2
Perfect score: 2041
Sequence: 1 MWNSSDANFSCYHESVLGYR.....FRQAYGSILKGRPSFHLH 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338	16.6	392	1 TRE1_DROME	Q9ndm2 drosophila
2	298	14.6	436	1 D2DR_MEIGA	O73810 meleagris g
3	291	14.3	442	1 D2D1_XENLA	P24628 xenopus lae
4	290	14.2	443	1 D2DR_HUMAN	P14416 homo sapien
5	290	14.2	443	1 D2DR_PANTR	P60026 pan troglod
6	288.5	14.1	466	1 A1AA_MOUSE	P97718 mus musculu
7	288.5	14.1	515	1 A1AB_MESAU	P18841 mesocricetu
8	288	14.1	444	1 D2DR_BOVIN	P20288 bos taurus
9	287.5	14.1	515	1 A1AB_RAT	P15823 rattus norv
10	287	14.1	443	1 D2DR_CERAE	P52702 cercopithec
11	286.5	14.0	519	1 A1AB_HUMAN	P35368 homo sapien
12	283.5	13.9	444	1 D2DR_MOUSE	P13953 mus musculu
13	281.5	13.8	466	1 A1AA_BOVIN	P18130 bos taurus
14	281	13.8	484	1 OAR2_LOCMI	Q25322 locusta mig
15	280	13.7	484	1 OAR1_LOCMI	Q25321 locusta mig
16	279.5	13.7	514	1 A1AB_MOUSE	P97717 mus musculu
17	278.5	13.6	466	1 A1AA_RABIT	O02824 oryctolagus
18	278.5	13.6	466	1 A1AA_RAT	P43140 rattus norv
19	274	13.4	466	1 A1AA_CAVPO	Q9wu25 cavia porce
20	274	13.4	466	1 A1AA_HUMAN	P35348 homo sapien
21	272.5	13.4	400	1 D3DR_HUMAN	P35462 homo sapien
22	272.5	13.4	463	1 D2DR_FUGRU	P53453 fugu rubrip
23	272	13.3	470	1 A1AA_ORYLA	Q91175 oryzias lat
24	271.5	13.3	562	1 A1AD_MOUSE	P97714 mus musculu
25	270.5	13.3	561	1 A1AD_RAT	P23944 rattus norv
26	268.5	13.2	400	1 D3DR_CERAE	P52703 cercopithec
27	267.5	13.1	446	1 D3DR_MOUSE	P30728 mus musculu
28	267.5	13.1	446	1 D3DR_RAT	P19020 rattus norv
29	267.5	13.1	583	1 ML1X_MOUSE	O88495 mus musculu
30	266	13.0	400	1 B3AR_MOUSE	P25962 mus musculu
31	266	13.0	425	1 OX1R_HUMAN	O43613 homo sapien
32	264.5	13.0	508	1 G101_HUMAN	Q9ep66 homo sapien
33	259	12.7	363	1 SH1E_PANTR	Q9n2b6 pan troglod

34	259	12.7	365	1 SH1E_HUMAN	P28566 homo sapien
35	259	12.7	452	1 GASR_RAT	P30553 rattus norv
36	257.5	12.6	576	1 A1AD_RABIT	O02666 oryctolagus
37	257	12.6	400	1 B3AR_RAT	P26255 rattus norv
38	255.5	12.5	416	1 OX1R_RAT	P56718 rattus norv
39	255	12.5	346	1 ML1C_CHICK	P49288 gallus gall
40	255	12.5	458	1 SH2C_HUMAN	P28335 homo sapien
41	254.5	12.5	458	1 A2AC_MOUSE	Q01337 mus musculu
42	254.5	12.5	458	1 A2AC_RAT	P22086 rattus norv
43	254	12.4	405	1 B3AR_SHEEP	Q9xt58 ovis aries
44	254	12.4	613	1 ML1X_HUMAN	Q13585 homo sapien
45	253	12.4	427	1 CCKR_RABIT	O97772 oryctolagus

ALIGNMENTS

RESULT 1
TRE1_DROME STANDARD; PRT; 392 AA.
ID TRE1_DROME Q95NV3; Q95NV9; Q9NKZ6; Q9W498;
AC Q9NDM2; Q95NV3; Q95NV9; Q9NKZ6; Q9W498;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Gustatory receptor Trehalose 1 (Trehalose receptor 1).
GN TRE1 OR CG3171.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=labial palps;
RX MEDLINE=20342437; PubMed=10884225;
RA Ishimoto H., Matsumoto A., Tanimura T.;
RT "Molecular identification of a taste receptor gene for trehalose in Drosophila.";
RL Science 289:116-119(2000).
RN [2]
RP SEQUENCE FROM N.A., FUNCTION, AND VARIANTS.
RC STRAIN=HG84, Shanghai, Singapore, Tananarive, w cv, and w cx;
RX MEDLINE=21450540; PubMed=11566105;
RA Ueno K., Ohta M., Morita H., Mikuni Y., Nakajima S., Yamamoto K., Isono K.;
RT "Trehalose sensitivity in Drosophila correlates with mutations in and expression of the gustatory receptor gene Gr5a.";
RL Curr. Biol. 11:1451-1455(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Flossler C., Gabrielson A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagrids.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nicholas large white; TISSUE=Brain;
RA Schnell S.A., You S., Foster D.N., el Halawani M.E.;
RT "Molecular cloning and tissue distribution of an avian D2 dopamine
RT receptor from the domestic turkey (Meleagris gallopavo).";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This is one of the five types (D1 to D5) of receptors
CC for dopamine. The activity of this receptor is mediated by G
CC proteins which inhibit adenylyl cyclase (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF056201; AAD03818.1; -;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 57 1 (POTENTIAL).
FT DOMAIN 58 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 94 2 (POTENTIAL).
FT DOMAIN 95 105 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 106 127 3 (POTENTIAL).
FT DOMAIN 128 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 171 4 (POTENTIAL).
FT DOMAIN 172 183 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 184 207 5 (POTENTIAL).
FT DOMAIN 208 366 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 367 390 6 (POTENTIAL).
FT DOMAIN 391 398 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 399 422 7 (POTENTIAL).
FT DOMAIN 423 436 CYTOPLASMIC (POTENTIAL).
FT DISULFID 104 179 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 15 15 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 436 AA; 49389 MW; 5FB13F684532C53B CRC64;

Query Match 14.6%; Score 298; DB 1; Length 436;
Best Local Similarity 25.5%; Pred. No. 2e-13;
Matches 116; Conservative 66; Mismatches 173; Indels 100; Gaps 17;

QY 2 WNSSDANFS-CYHESVLG----YRYVAVSWGVVAVTGTGNGVLTLLALAIQPKLRTRFN 56
DB 9 YNTGDRNWSEPNVNESSADQKPQNYAYVLLTLIFVI-VFGNVLVCMVAVSREKALQTTN 67

QY 57 LLIANLTLADLLYCTLLQPFSDTYLHL--HWRTGATFCRVFGLLLFASNSVSLTLCIL 114
DB 68 YLIVSLAVADLLVATLMPWVV--YLEVVGWGRFSRHCIDIFVTLDVMMCTASILNLCAI 125

QY 115 ALGRYLLIAHPKLPQVFSAGIVLALVS-TWVVGVSFAPLW-----PI 158
DB 126 SIDRYTAAAMPMLYNTRYSSKRRVTVMACVWLSFAISSPILFGLNKADERECIIANPA 185

QY 159 YIL-----VPVCTCSFDRIRGRPYTILMGIYFVLGLSSVGIFYCLIHQVKRAAQ 210
DB 186 FVYSSVVSFYVPFIVT-----LLVYVQIYMLVRRR-----KRHTKRSSH 226

QY 211 ALD-----QYKLQASIHNS-----HVARTDEAMPGRFQEL 241

Db 227 GLDSDTHAPLKDKCTHPENVKLGTVIVKSNQSGFQVNRKRCESHIKMEMEMMSSTSPPE 286
QY 242 DSRLASGSPSEGISSEPVSAATQTLE-----GDSSEVGDQINSKRAQMAEKSPPE 293
Db 287 RTIVKAAAPSNHQLVWPV-ASSRSTLDSPGKVEKNGHAK-----NLHTAKVFEIQSMNP 340
QY 294 ASAKAQPIKGARRAPDSSESSEFGKVTMCMFAVFLCFALSYIPFLLNILDARVQAPRVVHM 353
Db 341 GKTRSTLLKAMNRRKLSQOKEKATQMLAIVLGVFIICWLPPFITHILNMHCDNCNIPPAM 400
QY 354 LAANLTWL---NGCINPVLVYAMNQFRQAYGSIL 385
Db 401 YSA-FTWLGYNVSAVNPIIYTTTFNIEFRKAFMKIL 434

RESULT 3
D2D1_XENLA
ID_D2D1_XENLA STANDARD; PRT; 442 AA.
AC P24628;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE D(2) dopamine receptor 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91200321; PubMed=1826663;
RA Martens G.J.M., Molhuizen H.O.F., Groeneveld D., Roubos E.W.;
RT "Cloning and sequence analysis of brain cDNA encoding a Xenopus D2
RT dopamine receptor".
RL FEBS Lett. 281:85-89(1991).
CC -!- FUNCTION: This is one of the five types (D1 to D5) of receptors
CC for dopamine. The activity of this receptor is mediated by G
CC proteins which inhibit adenylyl cyclase. In xenopus D2r is
CC involved in the regulation of the melanotrope cells of the animal.
CC intermediate pituitary during background adaptation of the animal.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Brain; pituitary.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X59500; CAA42088.1; -;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 32 54 1 (POTENTIAL).
FT DOMAIN 55 65 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 66 91 2 (POTENTIAL).
FT DOMAIN 92 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 145 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 146 168 4 (POTENTIAL).
FT DOMAIN 169 180 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 181 204 5 (POTENTIAL).

[11] SEQUENCE FROM N.A. (ISOFORM 3).
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.,
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Kidd K.K.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [14]
RP VARIANT CYS-311.
RX MEDLINE=94071899; PubMed=7902708;
RA Itokawa M., Arinami T., Futamura N., Hamaguchi H., Toru M.;
RT "A structural polymorphism of human dopamine D2 receptor,
RT D2(Ser311->Cys)";
RL Biochem. Biophys. Res. Commun. 196:1369-1375(1993).
RN [15]
RP VARIANT MD ILE-154.
RX MEDLINE=99238502; PubMed=10220438;
RA Klein C., Brin M.F., Kramer P., Sena-Esteves M., de Leon D.,
RA Doheny D., Bressman S., Fahn S., Breakefield X.O., Ozelius L.J.;
RT "Association of a missense change in the D2 dopamine receptor with
RT myoclonus dystonia";
RL Proc. Natl. Acad. Sci. U.S.A. 96:5173-5176(1999).
CC -!- FUNCTION: This is one of the five types (D1 to D5) of receptors
CC for dopamine. The activity of this receptor is mediated by G
CC proteins which inhibit adenylyl cyclase.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=D2(Long);
CC IsoId=P14416-1; Sequence=Displayed;
CC Name=2; Synonyms=D2(Short);
CC IsoId=P14416-2; Sequence=VSP_001870;
CC Name=3; Synonyms=D2(Longer);
CC IsoId=P14416-3; Sequence=VSP_008511;
CC -!- DISEASE: It has been suggested that DRD2 is involved in
CC psychiatric disorders; especially in schizophrenia. It has also
CC been implicated in susceptibility to alcoholism.
CC -!- DISEASE: Defects in DRD2 are associated with myoclonus dystonia
CC (MD) [MIM:159900]; also known as myoclonic dystonia or alcohol-
CC responsive dystonia. MD is a movement disorder characterized by
CC involuntary lightning jerks and dystonic movements and postures
CC alleviated by alcohol. Inheritance is autosomal dominant.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M30625; AAA88024.1; -
DR EMBL; X51645; CAB56463.1; -
DR EMBL; X51646; CAB37869.1; -
DR EMBL; X51362; CAA35746.1; -
DR EMBL; M29066; AAA52761.1; -
DR EMBL; S62137; AAB26819.1; -
DR EMBL; S69899; AAB20571.1; -
DR EMBL; S58589; AAB26274.1; -
DR EMBL; S58577; AAB26274.1; JOINED.
DR EMBL; S58584; AAB26274.1; JOINED.
DR EMBL; S58586; AAB26274.1; JOINED.
DR EMBL; S58588; AAB26274.1; JOINED.
DR EMBL; AF176812; AAF61479.1; -
DR EMBL; AB065860; BAC06078.1; -
DR EMBL; AF050737; AAC78779.1; -
DR EMBL; BC021195; AAH21195.1; -
DR PIR; S08417; DYHUD2.
DR PDB; 1I15; 28-FEB-01.
DR Genew; HGNC:3023; DRD2.
DR MIM; 126450; -
DR MIM; 159900; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005882; C:intermediate filament; TAS.
DR GO; GO:0004952; F:dopamine receptor activity; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0007212; P:dopamine receptor signaling activity; TAS.
DR GO; GO:0007195; P:dopamine receptor, adenylate cyclase inhibi. . .; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR GO; GO:0007268; P:synaptic transmission; TAS.

Query Match 14.2%; Score 290; DB 1; Length 443;
Best Local Similarity 25.8%; Pred. No. 7.3e-13;
Matches 114; Conservative 65; Mismatches 183; Indels 80; Gaps 15;

QY 2 WNSSDANFSCVHESVLGYRYVAVSWGVVAVTGVGNVLTLLALAIQPKLRTRENLLIAN 61
Db 22 FNGSDGKADRPH-----YNYATLLTLLIAVI-VFGNVLCMAVSREKALQTTTNYLIVS 75

QY 62 LTLADLLYCTLLQPFSDTYLHL--HWRFGATFCRVFGLLLFASNSVILTCLIALGRY 119
Db 76 LAVADLLVATLVMPWV--YLEVVGWGWKFSRIHCDIFVTLDVVMCTASILNLCASIDRY 133

QY 120 LLIAHPKLPQVFSAGKIVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYT 179
Db 134 TAVAMPMLYNTRYSSKRRVTVMIS--IVWVLSFT-----ISCPLLFGLNNADQNE 181

QY 180 TILMGIYFVLGLSSVGIF-----YCLIHQRQ-----VKRAAQAL----- 212
Db 182 CIIANPAFVWYSSIVSFYVPFIVTLLVYIKIYIVLRRRKRVRNTKRSSRAFRAHLRAPLK 241

QY 213 -----DQYKLRQASIHNSN--HVARTEAMPGRFQELD-SRLASGGSPSEGISSEPVSA 262
Db 242 GNCSTHPEDMKLCTVIMKSNNGSFPVNRVRVEAARRAQELEMELSLSTSPERTRYSPIPPS 301

QY 263 TTQLEGDSSEVG-----DQINSKRAKQMAEKSPPEASAKAQPIKGARR 306
Db 302 HHQLTLPDPSSHGLHSTPDSAPAKPEKNGHAKDHPKIAKIFEIQTPMNGKTRTS-LKTMSR 360

QY 307 APDSSEFGKVTTRMCFVFLCFALSYPFLNLLILDARVQAPRVVHMLAANLTWL---NG 363
Db 361 RKLSSQKKEKKATQMLAIVLGVFIICWLPFFITHILNIHDCD-NIPPVLYSAFTWLGVNS 419

QY 364 CINPVLVYAMNRQFRQAYGSIL 385
Db 420 AVNPITYTTTFNIEPRKAFKIL 441

Query Match 14.2%; Score 290; DB 1; Length 443;
 Best Local Similarity 25.8%; Pred.No. 7.3e-13;
 Matches 114; Conservative 65; Mismatches 183; Indels 80; Gaps 15;

QY 2 WNSSDANFSCYHESVLGYRYVAVSGVAVTGTGNGVLTLLALAIQPKLRTFRNLLIAN 61
 Db 22 FNGSDGKADREH- - - - -YNYATLLTLLIAVI-VFGNVLVCMVAVSREKALQTTTNYLIVS 75
 QY 62 LTLADLLYCTLLQPFVSVDTYLHL--HWRTGATFCRVFGLLLFASNSVSLTLCIALGRY 119
 Db 76 LAVADLLVATLVMPWV--YLEVVGWKFHSRIHCDIFVTLDVNMCTASILNLCAISIDRY 133
 QY 120 LLIAHPKLPQVFSAGIVLALVSTWVGVSFAPLWPIYILVVPVCTCSFDRIRGRPYT 179
 Db 134 TAVAMPMLNTRYSSKRRVTVMIS--IVVLSFT-----ISCPLLFGLNNADQNE 181
 QY 180 TILMGIYFVLGLSSVGIF-----YCLIHQ-----VKRAAQAL----- 212
 Db 182 CIIANPAFVYSSIVSFYVPIVTLVYIKIYIVLRRRRKRVNTKRSSRAFAHLRAPLK 241
 QY 213 -----DQYKLRQASIHNSN--HVAETDEAMPGRFQELD-SRLASGGSPSEGISSEPVSA 262
 Db 242 GNCNTHPEDMKICTVIMKSNFVNRVVEAARRAQELEMELMSSTSPERTRYSPIPPS 301
 QY 263 TTQTLGDSSEVG-----DQINSKRAKQMAEKSPPEASAKAQPIKGARR 306
 Db 302 HHQLTLPDPSHHGLHSTPSPAKPEKNGHAKDHPKIAKIFEIQTMPNGKTRTS-LKTMSR 360
 QY 307 APDSSEFGKVTMCFVFLCFALSIYIPFLLNILDARVQAPRVVHMLAANLTWL---NG 363
 Db 361 RKLQQKEKKATQMLAIVLGVFIICWLPFFITHILNIHCHDC-NIPPVLYSAFTWLGYN 419
 QY 364 CINPVLYAAMNRQFRQAYGSIL 385
 Db 420 AVNPIIYTTFNIEFRKFLKIL 441

RESULT 6

ALAA_MOUSE STANDARD; PRT; 466 AA.
 ID ALAA_MOUSE
 AC P97718; O54913;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C adrenergic receptor).
 DE ADRA1A OR ADRA1C.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=CD-1; TISSUE=Brain, and Kidney;
 RX MEDLINE=98292316; PubMed=9630362;
 RA Xiao L., Scofield M.A., Jeffries W.B.;
 RT "Molecular cloning, expression and characterization of cDNA encoding a mouse alpha1A-adrenoceptor."
 RL Br. J. Pharmacol. 124:213-221(1998).
 RN [2]
 RP SEQUENCE OF 197-280 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96064818; PubMed=75955531;
 RA Alonso-Llamazares A., Zamanillo D., Casanova E., Ovalle S., Calvo P., Chinchetru M.A.;
 RT "Molecular cloning of alpha 1d-adrenergic receptor and tissue distribution of three alpha 1-adrenergic receptor subtypes in mouse."
 RT J. Neurochem. 65:2387-2392(1995).
 CC -!- FUNCTION: This alpha-adrenergic receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system. Its effect is mediated by G(q) and G(11) proteins.

RESULT 5
 D2DR_PANTR STANDARD; PRT; 443 AA.
 AC P60026;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE D(2) dopamine receptor.
 GN DRD2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate #130;
 RA Takahashi A., Hayasaka I., Noaki Y., Saitou N.;
 RT "Dopamine receptor D2 (DRD2) gene in Pan troglodytes."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: This is one of the five types (D1 to D5) of receptors for dopamine. The activity of this receptor is mediated by G proteins which inhibit adenylyl cyclase (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).
 DR EMBL; AB080609; BAC10668.1;
 DR EMBL; AB080603; BAC10668.1; JOINED.
 DR EMBL; AB080604; BAC10668.1; JOINED.
 DR EMBL; AB080605; BAC10668.1; JOINED.
 DR EMBL; AB080606; BAC10668.1; JOINED.
 DR EMBL; AB080607; BAC10668.1; JOINED.
 DR EMBL; AB080608; BAC10668.1; JOINED.
 DR PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEPT_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 38 60 1 (POTENTIAL).
 FT DOMAIN 61 71 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 72 97 2 (POTENTIAL).
 FT DOMAIN 98 108 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 109 130 3 (POTENTIAL).
 FT DOMAIN 131 151 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 152 174 4 (POTENTIAL).
 FT DOMAIN 175 186 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 187 210 5 (POTENTIAL).
 FT DOMAIN 211 373 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 374 397 6 (POTENTIAL).
 FT DOMAIN 398 405 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 406 429 7 (POTENTIAL).
 FT DOMAIN 430 443 CYTOPLASMIC (POTENTIAL).
 FT SITE 193 IMPLICATED IN CATECHOL AGONIST BINDING
 FT SITE 194 IMPLICATED IN RECEPTOR ACTIVATION
 FT SITE 197 IMPLICATED IN RECEPTOR ACTIVATION
 FT SITE 197 IMPLICATED IN RECEPTOR ACTIVATION
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 107 182 BY SIMILARITY.
 SQ SEQUENCE 443 AA; 50619 MW; 9BF8EA36C988A2E2 CRC64;

TRANSMEM 296 319 6 (POTENTIAL).
 FT DOMAIN 320 326 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 327 340 7 (POTENTIAL).
 FT DOMAIN 341 515 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 371 378 POLY-ARG.
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 118 195 BY SIMILARITY.
 FT LIPID 365 365 S-palmitoyl cysteine (Potential).
 FT MUTAGEN 293 293 A-X: CONFERS CONSTITUTIVE ACTIVITY.
 SQ SEQUENCE 515 AA; 56492 MW; 6DAF1576D1C1CE2D CRC64;

Query Match 14.1%; Score 288.5; DB 1; Length 515;
 Best Local Similarity 25.1%; Pred. No. 1.1e-12;
 Matches 103; Conservative 74; Mismatches 162; Indels 71; Gaps 14;

QY 2 WNS-SDANFSCVHE-----SVLGRYV--AVSWGVA--VTGTGNNVLTLLALAIQPKL 51
 Db 17 WGEKLDANFTGPNQTSNSTLPQLDVTRAISVGLVGLAFILFAIVGNILVILSVACNRHL 76

QY 52 RTRFNLLIANLTADLLYCTLLQPFSDVDTYHLHWRGTGATFCRVFGLLLFASNSVSLTL 111
 Db 77 RTPTNYFIVNLAIALDLSFTVLPFSATLEVLGYWVGLGRIFCDIWAADVLCCTASILSL 136

QY 112 CLIALGRYLLIAHPKLPQVFSAGKIVLALVSTWVG-VASFAPL--WPIYILVPVCTC 168
 Db 137 CAISIDRYIGVYSIQYPTLVTRRKAILALLSVWLSTVISIGPLLWK---EPAPND 192

QY 169 SFDRIIRGRPYTILMGI-YFVLGLSSVGFYCLHQRKAAQALDQYKLRQASIHSHV 227
 Db 193 KEGVTEEPFYALFSSLSFYIPLAVILWYCRVYIVAKRTTKNLEAGVMKEMS----- 246

QY 228 ARTDEAMPGRFQELDSRLASGGPSEGISSEPEVSAATTQTLEGDSSEVGDQINSKRAQMA 287
 Db 247 -----NSKELTLRIHKNFHE-----DTLSSTKAK--- 271

QY 288 EKSPPEASAKAOPKIGARRAPDSSESEFGKVTMCFVFLCFALSYIPFLL---LNILDAR 344
 Db 272 -GHNPRSSIAVKLFKFSRE-KKAATLGIWGM-----FILWLPFFIALPLGSLFST 322

QY 345 VQAPRVVHMLAANLTWNGCINPVLAAANRQFRQAYGSILKGRPSFHR 394
 Db 323 LKPPDAVFKVFWLGYFNLSCLNPIIYPCSSKEFKRAFMRILGQCQSGRR 372

RESULT 8
 D2DR_BOVIN STANDARD; PRT; 444 AA.
 ID D2DR_BOVIN STANDARD; PRT; 444 AA.
 AC P20288;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE D(2) dopamine receptor.
 GN DRD2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RX MEDLINE=90136899; PubMed=2137198;
 RA Chio C.L., Hess G.F., Graham R.S., Huff R.M.;
 RT "A second molecular form of D2 dopamine receptor in rat and bovine
 RT caudate nucleus."
 RL Nature 343:266-269(1990).
 CC -!- FUNCTION: This is one of the five types (D1 to D5) of receptors
 CC for dopamine. The activity of this receptor is mediated by G
 CC proteins which inhibit adenylyl cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

CC Name=Long; Sequence=Displayed;
 CC IsoId=P20288-1; Sequence=VSP_001869;
 CC Name=Short;
 CC IsoId=P20288-2; Sequence=VSP_001869;
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X51657; CAA35970.1; -;
 DR PIR; S08163; DYBOD2.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Alternative splicing.
 FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 38 60 1 (POTENTIAL).
 FT DOMAIN 61 71 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 72 97 2 (POTENTIAL).
 FT DOMAIN 98 108 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 109 130 3 (POTENTIAL).
 FT DOMAIN 131 151 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 152 174 4 (POTENTIAL).
 FT DOMAIN 175 186 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 187 210 5 (POTENTIAL).
 FT DOMAIN 211 374 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 375 398 6 (POTENTIAL).
 FT DOMAIN 399 406 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 407 430 7 (POTENTIAL).
 FT DOMAIN 431 444 CYTOPLASMIC (POTENTIAL).
 FT SITE 193 193 IMPLICATED IN CATECHOL AGONIST BINDING
 FT SITE 194 194 IMPLICATED IN RECEPTOR ACTIVATION
 FT SITE 197 197 IMPLICATED IN RECEPTOR ACTIVATION
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 107 182 BY SIMILARITY.
 FT VARSPLIC 242 270 Missing (in isoform Short).
 SQ SEQUENCE 444 AA; 50671 MW; 67437197629301C7 CRC64;
 Query Match 14.1%; Score 288; DB 1; Length 444;
 Best Local Similarity 26.8%; Pred. No. 1e-12;
 Matches 112; Conservative 65; Mismatches 181; Indels 60; Gaps 14;

QY 19 YRYVAVSWGVAVAVTGTGNNVLTLLALAIQPKLRTRFNLLIANLTADLLYCTLLQPFV 78
 Db 34 YNYAMLLTLIFVI-VFGNVLCMAVSREKALQTTTNYLVSLAVADLLVATLMPVWV 92

QY 79 DTYLHL--HWRTGATFCRVFGLLLFASNSVSLTCLIALGRYLLIAHPKLPQVFSAGK 136
 Db 93 --YLEVVGWVKFSRIHCDIFVTLDMCTASILNLCASIDRYTAVAMPMLYNTRYSSKR 150

QY 137 IVLALVSTWVGVASFAPLWPIYILVPVCTCSFDRIRGRPYTILMGI-----YFVLG 190
 Db 151 RVTVMIA--IVWLSTISCP--MLFGLNNTDQNECIANFAVYSSIVSFYVPFIVTL 206

QY 191 LSSVGIFYCLIHQ-----VKRAQAL-----DQYKLRQASIHNS---HVA 228
 Db 207 LVYIKIYIVLRRRKRVNTRKSSPAFRANLKAPLKGNCNTHPEDMKLCTVIMKNGSPV 266

QY 229 RTDEAMPGRFQELD-SRLASGGPSEGISSEPEVSAATTQTLEGDSSEVG----- 275

Db 267 RRRVEARRAQELEMESLSTSPPTTRYSPIPSHHQLTLDPDSHHGLSTPDSPAKPE 326

QY 276 -----DQINSKRAKQMAEKSPPEASAKAQPICKGARRAPDSSSBFGKVTRMCFVFLCFAL 330

Db 327 KNGHAKTVNPKIAKIFEIQMPNGKTRTS-LKTMSSRRKLSQOEKKATQMLAIVLGVFII 385

QY 331 SYIPFLLNLILDARVQAPRVVHMLAANLTWL---NGCINPVLYAAMNRQFRQAYGSIL 385

Db 386 CWLPFFITHILNIHDCD-NIPPVLYSAFTWLGYNVSAVNPIIYTFNIEFRKAFKIL 442

RESULT 9

ALAB RAT

ID AIAB RAT STANDARD; PRT; 515 AA.

AC P15823; Q63215;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor).

GN ADRA1B.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RX MEDLINE=90192094; PubMed=2156222;

RA Voigt M.M., Kispert J., Chin H.;

RT "Sequence of a rat brain cDNA encoding an alpha-1B adrenergic receptor.";

RL Nucleic Acids Res. 18:1053-1053(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91177889; PubMed=1706716;

RA Lomasney J.W., Cotecchia S., Lorenz W.-Y., Leung W.-Y., Schwinn D.A.,

RA Yang-Feng T.L., Brownstein M., Lefkowitz R.J., Caron M.G.;

RT "Molecular cloning and expression of the cDNA for the alpha 1A-

RT adrenergic receptor. The gene for which is located on human

RT chromosome 5.";

RL J. Biol. Chem. 266:6365-6369(1991).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=94010315; PubMed=8406017;

RA Gao B., Kunos G.;

RT "Isolation and characterization of the gene encoding the rat alpha 1B

RT adrenergic receptor.";

RL Gene 131:243-247(1993).

RN [4]

RP SEQUENCE OF 1-253 FROM N.A.

RX MEDLINE=95081407; PubMed=7989580;

RA Kanasaki M., Matsubara H., Murasawa S., Masaki H., Nio Y., Inada M.;

RT "cAMP responsive element-mediated regulation of the gene

RT transcripion of the alpha 1B adrenergic receptor by thyrotropin.";

RL J. Clin. Invest. 94:2245-2254(1994).

CC -!- FUNCTION: This alpha-adrenergic receptor mediates its action by

CC association with G proteins that activate a phosphatidylinositol-

CC calcium second messenger system.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X51585; CAA35934.1; --

DR EMBL; M60655; AAA63478.1; --

DR EMBL; L08610; AAA40647.1; --

DR EMBL; L08609; AAA40647.1; JOINED.

DR EMBL; D32045; BAA06806.1; --

DR PIR; JC1525; JC1525.

DR HSSP; P29274; 1MMH.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR PRINTS; PR00237; GPCRHOOPS.

DR PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECF1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Palmitate.

KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 46 70 1 (POTENTIAL).

FT DOMAIN 71 83 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 84 105 2 (POTENTIAL).

FT DOMAIN 106 115 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 116 141 3 (POTENTIAL).

FT DOMAIN 142 161 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 162 182 4 (POTENTIAL).

FT DOMAIN 183 201 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 202 224 5 (POTENTIAL).

FT DOMAIN 225 295 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 296 319 6 (POTENTIAL).

FT DOMAIN 320 326 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 327 340 7 (POTENTIAL).

FT DOMAIN 341 515 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 371 378 POLY-ARG.

FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 118 195 BY SIMILARITY.

FT LIPID 365 365 S-palmitoyl cysteine (Potential).

FT CONFLICT 114 116 GRI -> LSF (IN REF. 2).

FT CONFLICT 203 203 Y -> C (IN REF. 1 AND 4).

FT CONFLICT 207 207 S -> C (IN REF. 1 AND 4).

FT CONFLICT 306 306 C -> S (IN REF. 3).

FT CONFLICT 415 416 TQ -> QK (IN REF. 1).

FT CONFLICT 440 440 C -> Y (IN REF. 3).

FT CONFLICT 484 486 GDT -> ATA (IN REF. 1).

FT CONFLICT 493 493 T -> S (IN REF. 3).

FT CONFLICT 511 511 A -> G (IN REF. 1).

SQ SEQUENCE 515 AA; 56585 MW; AF0C3759F80C3135 CRC64;

Query Match 14.1%; Score 287.5; DB 1; Length 515;

Best Local Similarity 24.9%; Pred. No. 1.3e-12;

Matches 96; Conservative 71; Mismatches 151; Indels 67; Gaps 12;

QY 23 AVSWGVA---VTGTGNVLTLLALAIQPKLRTFRNLLIANLTADLLYCTLLQPFSD 79

Db 45 AISVGLVGAFLFAIVGNILVSVACNRHRTPTNYFIVNLAIDLSTVLPFSAT 104

QY 80 TYLHLHRTGATFCRVFGLLLFASNSVSLTCLIALGRYLLIAHPKLPQVFSAGIVL 139

Db 105 LEVLGYWVLGRIFCDIWAADVLCCTASILSICAISIDRYIGVYSQYPTLVTRKAIL 164

QY 140 ALVSTWVG-VASFAPL--WPIYILVPVCTCSFDRIRGRPYTTILMGI-YFVLGLSSVG 195

Db 165 ALLSVWVLSTVISIGPLLGWK---EPAPNDKCEGVTEEPFYALFSSLSGFYIPLAVIL 220

QY 196 IFYCLIHROVKRAQALDQYKLRQASIHNSHVARTDEAMPGRFOELDSRLASGSPSEGIS 255

Db 221 VMYCRVYIVAKRTTKNLEAGVWKEMS-----NSKELTLRHSKNFHE--- 262

QY 256 SEPVSAAATTQLEGDSSEVDQINSKRAKQMAEKSPPEASAKAQPIKGARRAPDSSSEFG 315

Db 263 -----DTLSSTKAK-----GHNPRSSIAVKLFKFSRE-KKAAKTLG 297

QY 316 KVTRMCFVFLCFALSYIPFLL---LNILDARVQAPRVVHMLAANLTWLNCGINPVLVAA 372

Db 298 IVVGM-----FILCWLPPFFIALPLGLSFSTLKPPDAVKVFWLGYFNSCLNPIIYPC 350

QY 373 MNRQFRQAYGSILK---RCPRSFHR 394

Db	351	SSKEFKRAFMRIILGQCRCGRRRRR	375	
RESULT 10				
D2DR_CERAE		STANDARD;	PRT;	443 AA.
ID	D2DR_CERAE			
AC	P52702;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	D(2) dopamine receptor.			
GN	DRD2.			
OS	Cercopithecus aethiops (Green monkey) (Grivet).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Cercopithecus.			
OX	NCBI_TaxID=9534;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=95302446; PubMed=7783157;			
RA	Thurkauf A., Hutchinson A., Peterson J., Cornfield L., Meade R.,			
RA	Houston K., Harris K., Ross P.C., Gerber K., Ramabhadran T.V.;			
RT	"2-phenyl-4-(aminomethyl)imidazoles as potential antipsychotic			
RT	agents. Synthesis and dopamine D2 receptor binding.";			
RL	J. Med. Chem. 38:2251-2255(1995).			
CC	-!- FUNCTION: This is one of the five types (D1 to D5) of receptors			
CC	for dopamine. The activity of this receptor is mediated by G			
CC	proteins which inhibit adenylyl cyclase.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC				
DR	EMBL; U18547; AAB60369.1; -			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm1; 1.			
DR	PRINTS; PR00237; GPCRHOODPSN.			
DR	PROSITE; PS00237; G PROTEIN RECEPTOR F1_1; 1.			
DR	PROSITE; PS00262; G PROTEIN RECEPTOR F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family.			
FT	DOMAIN 1 37	EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 38 60	1 (POTENTIAL).		
FT	DOMAIN 61 71	CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 72 97	2 (POTENTIAL).		
FT	DOMAIN 98 108	EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 109 130	3 (POTENTIAL).		
FT	DOMAIN 131 151	CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 152 174	4 (POTENTIAL).		
FT	DOMAIN 175 186	EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 187 210	5 (POTENTIAL).		
FT	DOMAIN 211 373	CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 374 397	6 (POTENTIAL).		
FT	DOMAIN 398 405	EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 406 429	7 (POTENTIAL).		
FT	DOMAIN 430 443	CYTOPLASMIC (POTENTIAL).		
FT	SITE 193 193	IMPLICATED IN CATECHOL AGONIST BINDING		
FT		(BY SIMILARITY).		
FT	SITE 194 194	IMPLICATED IN RECEPTOR ACTIVATION		
FT		(BY SIMILARITY).		
FT	SITE 197 197	IMPLICATED IN RECEPTOR ACTIVATION		
FT		(BY SIMILARITY).		
FT	CARBOHYD 5 5	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 17 17	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 23 23	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	DISULFID 107 182	BY SIMILARITY.		
RESULT 11				
ALAB_HUMAN		STANDARD;	PRT;	519 AA.
ID	ALAB_HUMAN			
AC	P35368;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor).			
GN	ADRA1B.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93016158; PubMed=1328250;			
RA	Ramarao C.S., Denker J.M., Perez D.M., Gaivin R.J., Riek R.P.,			
RA	Graham R.M.;			
RT	"Genomic organization and expression of the human alpha 1B-adrenergic			
RT	receptor.";			
RL	J. Biol. Chem. 267:21936-21945(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=94239386; PubMed=8183249;			
RA	Forray C., Bard J.A., Wetzel J.M., Chiu G., Shapiro E., Tang R.,			
RA	Lepor H., Hartig P.R., Weinshank R.L., Branchek T.A.,			
RA	Gluchowski C.;			
RT	"The alpha 1-adrenergic receptor that mediates smooth muscle			
RT	contraction in human prostate has the pharmacological properties of			
RT	the cloned human alpha 1c subtype.";			
RL	Mol. Pharmacol. 45:703-708(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			

Db 22 FNGSEKADPH-----YNYAMLLTLIFII-VFNVLCMAVSREKALQTTTNYLIVS 75
QY 62 LTLADLLYCTLLQPFSDTYLHL--HWRTGATFCRVFGLLLEASNSVSILTCLIALGRY 119
Db 76 LAVADLLVATLVMPWV--YLEVVGEWKFSDIRHCDIFVTLDMCTASILNLCAISIDRY 133
QY 120 LLIAHPKLPQVFSAGIVLALVS-TWVVGVSAPFAPLWPIYILVPVCTCSFDRIRGRPY 178
Db 134 TAVAMPMLYNTRYSSKRRVTVMIAVWVLSFTISCPL-----LFLNNTDQNECIANPA 188
QY 179 TTILMGI-----YFVLGLSSVGIFYCLIHQRQ---VKRAAQAL-----D 213
Db 189 FVYSSIVSFYVPIVITLLVYIKIYIVLRKRRKRVNTKRSSRAFRANLKTPLKGNCTHPE 248
QY 214 QYKLRQASTHSN-----HVARTEAMPGRFQELD-SRLASGPFSEGISSEPVSAATTQTL 267
Db 249 DMKLCVTVMKNSGSPFVNRMDAAR--RAQELEMEMLSSTSPERTRYSPIPPSHHOLT 306
QY 268 EGDSEVG-----DQINSKRAKQMAEKSPPEASAKAQPIKGARRAPDS 310
Db 307 LPDPSSHGLHSPDSPAPEKNGHAKIVNPIAKFFEIQTMPNGKTRTS-LKTMRSRRLS 365
QY 311 SSEFGKVTMCFPAVFLCFALSYPFLLNLILDARVQAPRVVHMLAANLTLWL---NGCINP 367
Db 366 QQKEKATQMLAIVLGVFIICWLPFFITHILNIHDCD-NIPPLYSAFTWLVGYVNSAVNP 424
QY 368 VLYAAMNQFRQAYGSIL 385
Db 425 IYTTFNIEERKAFMKIL 442

RESULT 13

ALAA BOVIN STANDARD; PRT; 466 AA.
ID ALAA BOVIN
AC P18130;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE adrenergic receptor).
GN ADRA1A OR ADRA1C.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90243698; PubMed=1970822;
RA Schwinn D.A., Lomasney J.W., Lorenz W., Szklut P.J., Premeau R.T. Jr.,
RA Yang-Feng T.L., Caron M.G., Lefkowitz R.J., Cotecchia S.;
RT "Molecular cloning and expression of the cDNA for a novel alpha 1-
RT adrenergic receptor subtype.";
RL J. Biol. Chem. 265:8183-8189(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92087349; PubMed=1966743;
RA Schwinn D.A., Cotecchia S., Lorenz W., Caron M.G., Lefkowitz R.J.;
RT "The alpha 1C-adrenergic receptor: a new member in the alpha 1-
RT adrenergic receptor family.";
RL Trans. Assoc. Am. Physicians 103:112-118(1990).
CC -1- FUNCTION: This alpha-adrenergic receptor mediates its action by
CC association with G proteins that activate a phosphatidylinositol-
CC calcium second messenger system. Its effect is mediated by G(q)
CC and G(11) proteins.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to licensee@isb-sib.ch).
CC -----
DR EMBL; J05426; AAA30374.1; --
DR PIR; A35375; A35375.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 27
FT TRANSMEM 28 51 1 (POTENTIAL).
FT DOMAIN 52 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 88 2 (POTENTIAL).
FT DOMAIN 89 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 122 3 (POTENTIAL).
FT DOMAIN 123 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 167 4 (POTENTIAL).
FT DOMAIN 168 181 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 182 205 5 (POTENTIAL).
FT DOMAIN 206 273 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 274 297 6 (POTENTIAL).
FT DOMAIN 298 305 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 306 329 7 (POTENTIAL).
FT DOMAIN 330 466 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 215 215 PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT DISULFID 99 176 BY SIMILARITY.
FT LIPID 345 345 S-palmitoyl cysteine (Potential).
SQ SEQUENCE 466 AA; 51466 MW; 77635153B39E85EC CRC64;

Query Match 13.8%; Score 281.5; DB 1; Length 466;
Best Local Similarity 23.0%; Pred. No. 2.9e-12;
Matches 95; Conservative 82; Mismatches 153; Indels 83; Gaps 13;

QY 3 NSSDANFSCYHESVLGYRYVAVSWGVVVA---VTGTGVNVLTLALLAIOPKLRTFRNLLI 59
Db 7 NASDSS-NCTHPPPPVNISKAILGLVILGGLILFVGLNVLVLSVACHRLHLSVTHYYI 65
QY 60 ANLTADLLYCTLLQPFSDTYLHLHWRTGATFCRVFGLLLEASNSVSILTCLIALGRY 119
Db 66 VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNVAAVDVLCCTASIMGLCIISIDRY 125
QY 120 LLIAHPKLPQVFSAGIVLALVSTWVG-VASFAPLWPIYILVP---VVCTCSFDRIRG 175
Db 126 IGVSYPRLRYPTIVTQKRGMLALLCVWALSLSVISIGPLFGWRQAPAPEDEITC-----QINE 180
QY 176 RPYTTILMGI-YFVLGLSSVGIFYCLIHQRVQAAQALDQYKLRQASHSNHVARTDEAM 234
Db 181 EPGYVLFSAALGSFYVPLTILVMYCRVYVVAKRERGL----- 218
QY 235 PGRFQELDSRLASGGPSEGISSEPVSAATTQLEGDSSEVGDIQINSKRAKQMAEKSPPEA 294
Db 219 -----KSGDKTD-----KSDSEQVTLRIHRKNA-QVGGSGVTSA 251
QY 295 SAK-----AQPIKGARRAPDSSEFGKVTMCFVFLCFALSYPFLLNLILDA---RVQA 347
Db 252 KNKTHFSVRLKFSREK-----KAAKTLGIVVGVFCVLCWLPLFFVMPICGFFPDFRP 303
QY 348 PRVWHMLAANLTWLNCGINPVLVYAAAMNQFRQAYGSI-----LKRGRPSFRL 395
Db 304 SETVFKIAFWLGLNLSINPIIYPCSSQEFKAFQNVLRIOQLRRKQSSKHTL 356

RESULT 14

OAR2_LOCM1
ID OAR2_LOCM1 STANDARD; PRT; 484 AA.
AC Q25322;

DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Putative tyramine receptor 2 (Tyr-Loc2).
 GN GCR2.
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Neuron;
 RA Vanden Broeck J.J.M.;
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 CC !- FUNCTION: G-protein coupled receptor for tyramine, a known
 CC neurotransmitter and neuromodulator and direct precursor of
 CC octopamine (By similarity).
 CC !- SUBCELLULAR LOCATION: Integral membrane protein.
 CC !- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X69521; CAA49269.1; -.
 DR HSSP; P29274; 1MMH.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 54
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 55 77
 FT DOMAIN 78 87
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 88 109
 FT DOMAIN 110 126
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 127 147
 FT DOMAIN 148 167
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 168 190
 FT DOMAIN 191 215
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 216 237
 FT DOMAIN 238 411
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 412 433
 FT DOMAIN 434 448
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 449 470
 FT DOMAIN 471 484
 FT CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 13 13
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 124 203
 FT POLY-PRO.
 FT DOMAIN 286 292
 FT ARG/LYS-RICH (BASIC).
 FT DOMAIN 294 307
 FT POLY-THR.
 FT DOMAIN 348 360
 FT SEQUENCE 484 AA; 53488 MW; 15C10608471D77CD CRC64;
 SQ

Query Match 13.8%; Score 281; DB 1; Length 484;
 Best Local Similarity 24.5%; Pred. No. 3.3e-12;
 Matches 111; Conservative 63; Mismatches 187; Indels 92; Gaps 17;
 QY 15 SVLGRYAVSWGVAVTG-----TVGNVLTLLALAIQPKLRTRFNLLIANLTAD 66
 Db 38 SVLGVRLAVPEWEVAVTAVSLSLIILITIVGNVLVLSVFTYKPLRIVQNFIVSLAVAD 97
 QY 67 LLYCTLLQPSVDYTLHLHWRTGATCFRVFGLLLFASNSVSLTCLIALGRYLLIAHPK 126
 Db 98 LTVAVLMPENVAVSLIQRWVGIIVCKMWLTCDVLCTASILNLCALDRYWAITDPI 157
 QY 127 LFPQVFSKGIIVLALVSTWV-VVASFAPL-----WPIYI--LVPVVTCSFDRIRGRPY 178

Db 158 NYAQKRTILRRVLAMIAGVWLLSGVSSPPLIGWNDWPFNDTTP-----COLTEEQGYVI 213
 QY 179 TTILMGYI---FVLGLSSVGIFYCLIHQVKRAA-----QALDQYKLRQA----- 220
 Db 214 YSSLGSFFIFLFIIMTIVYVEIFATKRRRLERAKASKLNSAMQQAQVAPSSVPSHDQ 273
 QY 221 ---SIHNSH-----VARTDEAMPGRF-----QELDSRLAS 247
 Db 274 ESVSSETNHNELPPPPAPPSPKERRKTKKSKKKQAAEEGRFLAPAMVAEDSVTDNSVS 333
 QY 248 GGP--SEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSP--EASAKAQP----- 300
 Db 334 VGPVAKNHLAEDGYTCTTTTTTTTTTAVTDSPRSRTASQKSTAPPTPVQPKSIPVYQF 393
 QY 301 IKGARRAPDSSEFEGKVTMCFVFLCFALSYPFLLLNIL-----DARVQAPRVVHMLA 355
 Db 394 IEEKQRI--SLSKERRAARTLGIIMGVFWVWLPFFLMYVIVPFCNPCKPSKLVNF-- 449
 QY 356 ANLTWL---NGCINPVLVYAAAMNROFRQAYGSIL 385
 Db 450 --ITWLGYNLSALNPIIYTIENLDFRRAFKLL 480
 RESULT 15
 OAR1_LOCM1
 ID OAR1 LOCM1 STANDARD; PRT; 484 AA.
 AC Q25321;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tyramine receptor 1 (Tyr-Loc1).
 GN GCRI.
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC TISSUE=Neuron;
 RX MEDLINE=95279966; PubMed=7760020;
 RA Vanden Broeck J.J.M., Vulsteke V., Huybrechts R., de Loof A.;
 RT "Characterization of a cloned locust tyramine receptor cDNA by
 RT functional expression in permanently transformed *Drosophila* S2
 RT cells."
 RL J. Neurochem. 64:2387-2395(1995).
 CC !- FUNCTION: G-protein coupled receptor for tyramine, a known
 CC neurotransmitter and neuromodulator and direct precursor of
 CC octopamine. The rank order of potency for agonists of this
 CC receptor is tyramine > naphazoline > tolazoline > DL-octopamine >
 CC dopamine > epinephrine > 5-hydroxytryptamine. For antagonists, the
 CC rank order is yohimbine > chlorpromazine > mianserin >
 CC phentolamine > metoclopramide.
 CC !- SUBCELLULAR LOCATION: Integral membrane protein.
 CC !- TISSUE SPECIFICITY: Present mainly in the central nervous system,
 CC especially in the supra- and suboesophageal, thoracic and
 CC abdominal ganglia. Not found in the distal part of optic lobes.
 CC !- DEVELOPMENTAL STAGE: Expressed in the nervous system by the
 CC first larval stage.
 CC !- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X69520; CAA49268.1; -.
 DR PIR; S58868; S58868.
 DR HSSP; P29274; 1MMH.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 07:26:02 ; Search time 131 Seconds
(without alignments)
953.780 Million cell updates/sec

Title: US-10-029-436-2
Perfect score: 2041
Sequence: 1 MWNSDANFSCYHESVLGYR.....FRQAYGSILKGRPSFRLH 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2041	100.0	396	4 Q9NQS5	Q9nqs5 homo sapien
2	1749	85.7	396	11 Q8CIM5	Q8cim5 mus musculu
3	1748	85.6	396	11 Q99MX9	Q99mx9 mus musculu
4	378	18.5	670	5 Q9W534	Q9w534 drosophila
5	378	18.5	670	5 Q8MRD0	Q8mrd0 drosophila
6	378	18.5	670	5 Q77270	Q77270 drosophila
7	309	15.1	572	5 Q77269	Q77269 drosophila
8	309	15.1	572	5 Q9W533	Q9w533 drosophila
9	295.5	14.5	361	5 Q8WPA2	Q8wpa2 bombyx mori
10	289	14.2	414	6 Q9GK99	Q9gk99 canis famil
11	289	14.2	459	11 Q8CGI5	Q8cgi5 mus musculu
12	289	14.2	515	11 Q9DBL0	Q9db10 mus musculu
13	288.5	14.1	427	11 Q8BUE5	Q8bue5 mus musculu
14	288.5	14.1	466	11 Q8BV77	Q8bv77 mus musculu
15	286.5	14.0	564	5 Q23013	Q23013 caenorhabdi
16	285	14.0	414	6 Q9GKA0	Q9gka0 canis famil

17	285	14.0	452	13 Q7T1A1	Q7t1a1 brachydanio
18	285	14.0	454	13 Q8AWE1	Q8awe1 brachydanio
19	283.5	13.9	464	13 Q90WQ6	Q90wg6 oncorhynchu
20	282	13.8	518	6 Q9MYI8	Q9myi8 oryctolagus
21	281	13.8	461	13 Q90WQ7	Q90wg7 oncorhynchu
22	280	13.7	466	4 Q96RE8	Q96re8 homo sapien
23	279.5	13.7	466	6 Q9TSW7	Q9tsw7 sus scrofa
24	278.5	13.6	423	5 Q964D4	Q964d4 periplaneta
25	278.5	13.6	425	6 Q9MZU2	Q9mzu2 oryctolagus
26	278.5	13.6	429	6 Q9MZU3	Q9mzu3 oryctolagus
27	278.5	13.6	443	6 Q9GJU1	Q9gju1 canis famil
28	276.5	13.5	420	13 Q8JG01	Q8jg01 fugu rubrip
29	274	13.4	429	4 Q13729	Q13729 homo sapien
30	274	13.4	455	4 Q60451	Q60451 homo sapien
31	274	13.4	499	4 Q13675	Q13675 homo sapien
32	273	13.4	448	13 Q8AWE0	Q8awe0 brachydanio
33	273	13.4	466	4 Q9UD63	Q9ud63 homo sapien
34	270.5	13.3	511	13 Q9PSA7	Q9psa7 fugu rubrip
35	270	13.2	419	5 Q77254	Q77254 boophilus m
36	270	13.2	425	4 Q9HBV6	Q9hbv6 homo sapien
37	269.5	13.2	559	11 Q9QW71	Q9qw71 rattus sp.
38	267.5	13.1	400	6 Q8MKJ0	Q8mkj0 cebus apell
39	267	13.1	399	4 Q13167	Q13167 homo sapien
40	264.5	13.0	357	5 Q9NBC8	Q9nbc8 drosophila
41	263	12.9	471	13 Q8UUG8	Q8uug8 tetraodon f
42	260.5	12.8	388	13 Q8JG07	Q8jg07 fugu rubrip
43	259	12.7	363	6 Q9N2B6	Q9n2b6 pan troglod
44	259	12.7	363	6 Q9N2B5	Q9n2b5 gorilla gor
45	258	12.6	437	13 Q7T1A2	Q7t1a2 brachydanio

ALIGNMENTS

RESULT 1
Q9NQS5
ID Q9NQS5 PRELIMINARY; PRT; 396 AA.
AC Q9NQS5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inflammation-related G protein-coupled receptor EX33 (Orphan G
DE protein-coupled receptor 84) (Putative G-protein coupled
DE receptor).
DE EX33 OR GPR84 OR GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yousefi S., Cooper P., Mueck B., Potter S., Jarai G.;
RT "Targeted Identification and Expression Analysis of Chemokine
RT Receptors in Neutrophils.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T., Schaller H.C., Hellebrand S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in
RT the discovery of new g-protein coupled receptors.";
RL J. Mol. Biol. 307:799-813(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF282693; AAF91467.1; --
DR EMBL; AF237762; AAK01857.1; --
DR EMBL; BC020614; AAH20614.1; --
DR EMBL; AB083586; BAB89299.1; --
DR Genew; HGNC:4535; GPR84.
DR GO; GO:0016526; F:G-protein coupled receptor activity, unknown. . .; NAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 396 AA; 43705 MW; BEEA467DFEB7520B CRC64;
Query Match 100.0%; Score 2041; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.9e-162;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVVAVTGTGNNVLTLLALAIQPKLRTRENLLIA 60
Db 1 MNSSDANFSCYHESVLGYRYVAVSWGVVAVTGTGNNVLTLLALAIQPKLRTRENLLIA 60
QY 61 NLTADLLYCTLLQPFSSVDTYLHLHWRTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
Db 61 NLTADLLYCTLLQPFSSVDTYLHLHWRTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
QY 121 LIAHPKLFPOVFSAGIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLFPOVFSAGIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY 181 ILMGIYFVLGLSSVGIFYCLIHROVKRAAALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
Db 181 ILMGIYFVLGLSSVGIFYCLIHROVKRAAALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
QY 241 LDSRLASGGPSEGISSEPVSAATTQILEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
Db 241 LDSRLASGGPSEGISSEPVSAATTQILEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
QY 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
RESULT 2
Q8CIMS PRELIMINARY; PRT; 396 AA.
AC Q8CIMS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G protein-coupled receptor 84.
GN GPR84.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC023249; AAH23249.1; --
DR MGD; MGI:1934129; Gpr84.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.

DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 396 AA; 43717 MW; 80F0601CBB4B1B03 CRC64;
Query Match 85.7%; Score 1749; DB 11; Length 396;
Best Local Similarity 85.6%; Pred. No. 5.2e-138;
Matches 339; Conservative 19; Mismatches 38; Indels 0; Gaps 0;
QY 1 MNSSDANFSCYHESVLGYRYVAVSWGVVAVTGTGNNVLTLLALAIQPKLRTRENLLIA 60
Db 1 MNSSDANFSCYHESVLGYRYVAVSWGVVAVTGTGNNVLTLLALAIQPKLRTRENLLIA 60
QY 61 NLTADLLYCTLLQPFSSVDTYLHLHWRTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
Db 61 NLTADLLYCTLLQPFSSVDTYLHLHWRTGATFCRVFGLLLFASNSVSILTCLIALGRYL 120
QY 121 LIAHPKLFPOVFSAGIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
Db 121 LIAHPKLFPOVFSAGIVLALVSTWVGVSFAPLWPIYILVPVCTCSFDRIRGRPYTT 180
QY 181 ILMGIYFVLGLSSVGIFYCLIHROVKRAAALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
Db 181 ILMGIYFVLGLSSVGIFYCLIHROVKRAAALDQYKLRQASIHSHNHVARTDEAMPGRFOE 240
QY 241 LDSRLASGGPSEGISSEPVSAATTQILEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
Db 241 LDSRLASGGPSEGISSEPVSAATTQILEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP 300
QY 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360
Db 301 IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLTW 360
QY 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
Db 361 LNCINPVLVYAMNRQFRQAYGSILKRGPRSFHRLH 396
RESULT 3
Q99MX9 PRELIMINARY; PRT; 396 AA.
AC Q99MX9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Orphan G protein-coupled receptor 84.
GN GPR84.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RX MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T., Schaller H.C., Hellebrand S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in
the discovery of new g-protein coupled receptors.";
RL J. Mol. Biol. 307:799-813(2001).
DR EMBL; AF272948; AAK01859.1; --
DR MGD; MGI:1934129; Gpr84.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 396 AA; 43731 MW; D7536A2FB96462D8 CRC64;
Query Match 85.6%; Score 1748; DB 11; Length 396;
Best Local Similarity 85.4%; Pred. No. 6.3e-138;

QY 67 LLYCTLLQPFSDVTLHLHWRGTATFCRVFGLLLFASNSVSLTLCLIALGRYLLIAHPK 126
 Db 83 LLFCALVLPFQGLRFVQGTWRHGLVLCRLIPFIQYGNIGVSLLCIAMITINRYVMITHHG 142

QY 127 LFPQVFSAGIVLALVSTWVGVASFAPL-----WPIYILVPVVTCS-FDRIRGRPYTTI 181
 Db 143 LYARIYKRHWIAVMAACWLFSGYGMQLPTLLGEWGRFGYDSRLQTCSIMTDDHGHSSKTT 202

QY 182 LMGIFYFVLGLSSVGIFCYLIHRQVKRAAQALDQYKLRQASIHNSHVARTDEAMPGRFQEL 241
 Db 203 LFITAFVIPCLVIACYAKIFWVVKSEORLKRHATKQNSI-----PNNLRPL 250

QY 242 DSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP- 300
 Db 251 AS-TGSGALPSGAECP-----SNRVSSDSSSFSDVPETAP---SGKQOPT 294

QY 301 -IKGARRAPDSSSEFGKVTMCMFAVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLT 359
 Db 295 RVKDQREVRARNEW-RITKMVLAIFLSFVVCYLPITIVKVADKNVEHPS-LHICSYILL 352

QY 360 WLNCGINPVLAAAMNRQFRQAYGSIL 385
 Db 353 YLSACINPIIYVIMNKQYKAYKTIV 378

RESULT 5
 Q8MRDO PRELIMINARY; PRT; 670 AA.

ID Q8MRDO
 AC Q8MRDO;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE RE06985P.
 GN EG:22E5.11 OR CG4322.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY121660; AAMS1987.1; --
 DR FlyBase; FBgn0025631; EG:22E5.11.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 SQ SEQUENCE 670 AA; 71917 MW; 3EB65941C517D1D CRC64;

Query Match 18.5%; Score 378; DB 5; Length 670;
 Best Local Similarity 26.4%; Pred. No. 5.3e-23;
 Matches 102; Conservative 79; Mismatches 165; Indels 40; Gaps 10;

QY 7 ANFSCYHESVGLGYRYVAVSWGVVAVTGTGNVLTLLALAIQPKLRTFRNLLIANLTAD 66
 Db 26 ADATGFSQSLLTFAAVMT---FLIMIVGICGNLLTVALLKCPKVRNVAAAFIISLCIAD 82

QY 67 LLYCTLLQPFSDVTLHLHWRGTATFCRVFGLLLFASNSVSLTLCLIALGRYLLIAHPK 126
 Db 83 LLFCALVLPFQGLRFVQGTWRHGLVLCRLIPFIQYGNIGVSLLCIAMITINRYVMITHHG 142

QY 127 LFPQVFSAGIVLALVSTWVGVASFAPL-----WPIYILVPVVTCS-FDRIRGRPYTTI 181
 Db 143 LYARIYKRHWIAVMAACWLFSGYGMQLPTLLGEWGRFGYDSRLQTCSIMTDDHGHSSKTT 202

QY 182 LMGIFYFVLGLSSVGIFCYLIHRQVKRAAQALDQYKLRQASIHNSHVARTDEAMPGRFQEL 241
 Db 203 LFITAFVIPCLVIACYAKIFWVVKSEORLKRHATKQNSI-----PNNLRPL 250

QY 242 DSRLASGGPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP- 300
 Db 251 AS-TGSGALPSGAECP-----SNRVSSDSSSFSDVPETAP---SGKQOPT 294

QY 301 -IKGARRAPDSSSEFGKVTMCMFAVFLCFALSYPFLLLNILDARVQAPRVVHMLAANLT 359
 Db 295 RVKDQREVRARNEW-RITKMVLAIFLSFVVCYLPITIVKVADKNVEHPS-LHICSYILL 352

QY 360 WLNCGINPVLAAAMNRQFRQAYGSIL 385
 Db 353 YLSACINPIIYVIMNKQYKAYKTIV 378

RESULT 6
 O77270 PRELIMINARY; PRT; 670 AA.

ID O77270
 AC O77270;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE EG:22E5.11 protein.
 GN EG:22E5.11 OR CG4322.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Murphy L., Harris D., Barrell B.;
 RT "Sequencing the distal X chromosome of Drosophila melanogaster."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Benos P.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031765; CAA21123.1; --
 DR PIR; T13739; T13739.
 DR FlyBase; FBgn0025631; EG:22E5.11.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 SQ SEQUENCE 670 AA; 71918 MW; 1E8022C0882A9E41 CRC64;

Query Match 18.5%; Score 378; DB 5; Length 670;
 Best Local Similarity 26.4%; Pred. No. 5.3e-23;
 Matches 102; Conservative 79; Mismatches 165; Indels 40; Gaps 10;

QY 7 ANFSCYHESVGLGYRYVAVSWGVVAVTGTGNVLTLLALAIQPKLRTFRNLLIANLTAD 66
 Db 26 ADATGFSQSLLTFAAVMT---FLIMIVGICGNLLTVALLKCPKVRNVAAAFIISLCIAD 82

QY 67 LLYCTLLQPFSDVTLHLHWRGTATFCRVFGLLLFASNSVSLTLCLIALGRYLLIAHPK 126
 Db 83 LLFCALVLPFQGLRFVQGTWRHGLVLCRLIPFIQYGNIGVSLLCIAMITINRYVMITHHG 142

QY 127 LFPQVFSAGIVLALVSTWVGVASFAPL-----WPIYILVPVVTCS-FDRIRGRPYTTI 181
 Db 143 LYARIYKRHWIAVMAACWLFSGYGMQLPTLLGEWGRFGYDSRLQTCSIMTDDHGHSSKTT 202

QY 182 LMGIVFVLGLSSVGIFYCLIHROVKRAAQAALDQYKLRQASIHSHNHVARTDEAMPGRFQEL 241
Db 203 LFITAFVIPCLVIIACYAKIFWVVKSEQLRKHATKQNSI-----PNNLRPL 250
QY 242 DSRLASGSPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEASAKAQP- 300
Db 251 AS-TGSGALPSGAECQP-----SNRVSSDSSSFSDVPETAP---SGKQOPT 294
QY 301 -IKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNILDARVQAPRVVHMLAANLT 359
Db 295 RVKDQREVRAKRNEW-RITKMVLAIFLSFVVCYLPITIVKVADKNVEHPS-LHICSYILL 352
QY 360 WLNGCINPVLVYAAMNRQFRQAYGSIL 385
Db 353 YLSACINPIYVIMNKQYRKAYKTIV 378

RESULT 7
O77269
ID O77269 PRELIMINARY; PRT; 572 AA.
AC O77269;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE EG:22E5.10 protein.
GN EG:22E5.10 OR CG4313.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Benos P.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031765; CAA21124.1; --
DR PIR; T13740; T13740.
DR FlyBase; FBgn0025632; EG:22E5.10.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 572 AA; 64304 MW; 8E19D28CB61CCD26 CRC64;

Query Match 15.1%; Score 309; DB 5; Length 572;
Best Local Similarity 22.4%; Pred. No. 2.6e-17;
Matches 102; Conservative 83; Mismatches 180; Indels 90; Gaps 10;

QY 9 FSCYHESVLGYRYVAVSWGVVAVTGTGVNVLTLALAIQPKLRFNFNLLIANLTLDLL 68
Db 100 FEGYSDELLTIAWVAC---IVFIIIVGPGNLLTIVALSRGRQTNSTAIFINLSCSDLL 156
QY 69 YCTLLQPFSDVTYHLHWRTGATFCRVFGLLFFASNVSILTLCLIALGRYLLIAHPKLF 128
Db 157 FGCNPLPLAASPFKRAWTHSDLLCLRFLPMLRYGLLAVSLLSVLITINRYIIAHPRQY 216
QY 129 PQVFSAKGIVLALVSTWVVGVSFAP----LWPIYILVPVCTCSFDRIR-GRPYTTILM 183
Db 217 PRIYQRRYLALMVAGTWITTFSIMIPTWRGVWGIFGLDVSIGSCSINHRYGRSPKEFLF 276
QY 184 GIYFVLGLSSVGIFYCLIHROVKRAA-----QALDQYKLRQ 219
Db 277 IAAFVWPCICIVCYARIFLLVRKAAIRACTAGKTNVSDVTPSSAPQHQIQAMATPKKPE 336

QY 220 ASIHSHNHVARTDEAMPGRFQELDSRLASGSPSEGISSEPVSAATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEA----- 260
Db 337 KVTSS--GEANEPIAGRPFFVVEENLAYIDDNASTDLSLPISYSIRRRDQDQOPPPVDANV 394
QY 261 -----AATTQTLEGDSSEVGDQINSKRAKQMAEKSPPEA----- 294
Db 395 VLKEREKERDRDQEKVSLGRSQTQLEMGKTHGKNPITTSLRRTSTFRFSRKSHPYASMGN 454
QY 295 SAKAQPIKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNILDARVQAPRVVH-- 352
Db 455 TSNASSIYPGR---MSAKDRRLKMLIVFVFWFVICYLPITIVAKIWSATE----VHWF 506
QY 353 -MLAANLTWLNGCINPVLVYAAMNRQFRQAYGSILK 386
Db 507 NIAGYLLIYLTTCINPLIYVLMSEYRRAYWNLLR 541

RESULT 8
Q9W533
ID Q9W533 PRELIMINARY; PRT; 572 AA.
AC Q9W533;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE EG:22E5.10 protein.
GN EG:22E5.10 OR CG4313.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Niklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AB003422; AAF45710.1; -.
 DR FlyBase; FBgn0025632; EG:22E5.10.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 572 AA; 64317 MW; 8E19D4E0EE2122C6 CRC64;

Query Match 15.1%; Score 309; DB 5; Length 572;
 Best Local Similarity 22.4%; Pred. No. 2.6e-17;
 Matches 102; Conservative 83; Mismatches 180; Indels 90; Gaps 10;

QY 9 FSCYHESVLGRYVAVSVGVAVTGTGCVNLTLLALAIQPKLRTRFNLLIANLTUADLL 68
 Db 100 FEGYSDELTIWVAC--IVFIIIVGPGNLTIVALSRGTRNSTAIFINLSCSDDL 156

QY 69 YCTLLQPFSDVDTYHLHWRTGATFCRVFGLLLFASNSVSILTCLIALGRYLLIAHPKLF 128
 Db 157 FGCNPLPLAASSTFKERAWTHSDLLCLRPMLRYGLLAVSLSLITINRYIIIAHPQY 216

QY 129 PQVFSAGIVLALVSTWVGVAFAFAP---LWPIYILVPVCTCSFDRIR-GRPYTTILM 183
 Db 217 PRIYQRRYLALWAGTWITTFIMPTWRGVWGIFGLDVSIGSCSIMHDIRYGRSPKEFLF 276

QY 184 GIYFVLGLSSVGIFYCLIHQRVRAA-----QALDQYKLRQ 219
 Db 277 IAAFMVPCICIVICYARIFLLVRKAIRAGTAGKTNVSDVTPSSAPQHAIQAMATPKKPE 336

QY 220 ASIHSNHVARTDEAMPGRFQELDSRLASGGPSEGISSEPV----- 260
 Db 337 KVTTS--GEANEPIAGRPFVVEENLAYIDNASTDSLPSYSIRRRDQDQPPVPDANV 394

QY 261 -----AATTQLEGDSSEVGDQINSKRAQMAEKSPPEA----- 294
 Db 395 VLKEREKERDRDQEKVSLGRSQTLEMGKTHGKNPITTSRTTSFTFSRPSKSHVYASMG 454

QY 295 SAKAQPIKARRAPDSSEFGKVTMCFVFLCFALSYPFLLNILDARVQAPRVVH-- 352
 Db 455 TSNASSIYPCR---MSAKORRLKMLVIFVWFVICYLPITVAKWSATE----VHWF 506

QY 353 -MLAANLTWLCINPVLVYAAKNRQFRQAYGSILK 386
 Db 507 NIAGYLLIYLTTCINPLIYVLMSEYRWAYNLLR 541

RESULT 9
 Q8WPA2 PRELIMINARY; PRT; 361 AA.
 AC Q8WPA2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Allatostatin receptor BAR.
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Lyon 200 BA/Lyon 300 AB;
 RX MEDLINE=21601656; PubMed=11590150;
 RA Secher T.; Lenz C.; Cazzamali G.; Sorensen G.; Williamson M.;
 RA Hansen G.N.; Svane P.; Grimmelikhuijzen C.J.P.;

RT "Molecular Cloning of a Functional Allatostatin Gut/Brain Receptor and
 RT an Allatostatin Preprohormone from the Silkworm Bombyx mori.";
 RL J. Biol. Chem. 276:47052-47060(2001).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF303370; AAL47056.1; -.
 DR EMBL; AF303368; AAL47056.1; JOINED.
 DR EMBL; AF303369; AAL47056.1; JOINED.
 DR EMBL; AF254742; AAG44631.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 361 AA; 40478 MW; 63C2B2846FC3010A CRC64;

Query Match 14.5%; Score 295.5; DB 5; Length 361;
 Best Local Similarity 22.4%; Pred. No. 1.9e-16;
 Matches 88; Conservative 61; Mismatches 111; Indels 133; Gaps 10;

QY 20 RYVAVSWGUVVAVTGTGCVNLTLLALAIQPKLRTRFNLLIANLTUADLLYCTLLQPFSDV 79
 Db 43 RVVPIFFG-FIGIVGLVGNALVVLVAANPGMRSTNLLINLAVADLLFVFCVPFTAT 101

QY 80 TYLHLHWRTGATFCRVFGLLLFASNSVSILTCLIALGRYLLIAHPKLPQVFSAGIVL 139
 Db 102 DYVMPRPFGDWCKVQVQYFIVVTAHASVYTLVMSLDREMAVVHPIASMSIRTEKNALL 161

QY 140 ALVSTWVVGVSFAFAPLWPIYILVPVVC-----TCSFDRIRGRPYTTILMGI 185
 Db 162 AIACIWWVILTTPVPG-----ICHGEREYSYFNRNHSVCVFLERGYSKLGFQMSF 213

QY 186 Y---FVLGLSSVGIFY-CLIHQRVQKRAAQALDQYKLRQASHNSHVARTDEAMPGRFQEL 241
 Db 214 FLSSYVPLALISVLYMCM----- 233

QY 242 DSRLASGGPSEGISSEPVSAATTQLEGDSSEVGDQINSKRAQMAEKSPPEASAKAQPI 301
 Db 234 -TRLWKSAPGGRVSAE-----SRRGRK----- 254

QY 302 KGARRAPDSSESSEFGKVTMCFVFLCFALSYPFLLNILDA-----RVQAPRVVH 352
 Db 255 -----KVTMVMVVVVVFAVVCWCPCIIILLVKALNKYHITYFTVTAQIVSH 300

QY 353 MLAANLTWLCINPVLVYAAKNRQFRQAYGSIL 385
 Db 301 VLA---YMNVCNPNVLYAFLENFRVAFKVM 329

RESULT 10
 Q9GK99 PRELIMINARY; PRT; 414 AA.
 AC Q9GK99;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Dopamine D2 receptor short isoform.
 GN DRD2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20510028; PubMed=11054572;
 RA Myeong H.; Jeoung D.; Kim H.; Ha J.H.; Lee Y.; Kim K.H.; Park C.;
 RA Kaang B.;
 RA "Genomic analysis and functional expression of canine dopamine D2

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawajiri H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RL Nature 420:563-573(2002).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AK004891; BAB23647.1; -.
 DR EMBL; AK043877; BAC31691.1; -.
 DR MGD; MGI:104774; Adra1b.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOODOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 515 AA; 56497 MW; 69D724E9978F81C1 CRC64;
 Query Match 14.2%; Score 289; DB 11; Length 515;
 Best Local Similarity 25.2%; Pred. No. 1.1e-15;
 Matches 104; Conservative 74; Mismatches 161; Indels 74; Gaps 15;
 QY 2 WNS-SDANFSCYHE---SVLGRIYV--AVSWGVVVA---VTGTGNNVLTLLALAIQPKL 51
 Db 17 WGEKLDANFTGPNQTSNSTLPQDVTTRAISVGLVGLAFILFAIVGNILVILSVACNRHL 76
 QY 52 RTRFNLLIANLTADLLYCTLLQPFSDVTYHLHWRTGATFCRVFGLLLFASNSVSIITL 111
 Db 77 RPTNYFIYNLAIDALLSFTVLPESATLEVGLYVWVLTGRIFCDIAAVDVLCTASISL 136
 QY 112 CLIALGRYLLIAHPKLFPOQVFSAGKIVLALVSTWVG-VASFAPL--WPIYILPVVCTC 168
 Db 137 CAISIDRYIGVRYSLQYPTLVTRRKAILALLSVVLTSTVIGPLLGWK---EPAPND 192
 QY 169 SFDRIRGRPYTILMGI-YFVLGLSSVGIFYCLIHQVRAQAALDQYKLRQASIHNV 227
 Db 193 KEGVTTEEFYALFSSLSGFIPLAVILMYCRVYIVAKTKNLEAGVMKEMS----- 246
 QY 228 ARTDEAMPGRFQELDSRLASGPGSEGISSEPVSAATTQLEGDSSEVGDQINSKRAQMA 287
 Db 247 -----NSKELTLRIHSKNFHE-----DTLSSTKAK--- 271
 QY 288 EKSPPEASAKAQPIKGARRAPDSSEFGKVTMCFVFLCFALSYPFL--LNILDAR 344
 Db 272 -GHNPRSSIAVKLFKFSRE-KKAATLGIIVGM-----FILCWLPPFFIALPLGSLEST 322
 QY 345 VQAPRVVHMLAANLTWNLGNCINPVLVYAMNRQFQAYGSIK--RGPRSFHR 394
 Db 323 LKPPDAVFKVFWLGYFNLSCLNPIIYPCSSKEFKRAFMRILGCQCRGRRRR 375
 RESULT 13
 Q8BUE5 PRELIMINARY; PRT; 427 AA.
 AC Q8BUE5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adrenergic receptor.
 GN ADRA1A.
 RA Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RL Nature 420:563-573(2002).
 DR EMBL; AK085653; BAC39495.1; -.
 DR MGD; MGI:104773; Adra1a.
 DR GO; GO:0008217; P:regulation of blood pressure; IMP.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOODOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 SQ SEQUENCE 427 AA; 47515 MW; 3810E9D5F5A09317 CRC64;
 Query Match 14.1%; Score 288.5; DB 11; Length 427;
 Best Local Similarity 23.1%; Pred. No. 9.2e-16;
 Matches 97; Conservative 78; Mismatches 148; Indels 97; Gaps 14;
 QY 3 NSSDANFSCYHESVLYGYRYVAVSWGVVVA---VTGTGNNVLTLLALAIQPKLRTFNLLI 59
 Db 7 NASEGS-NCTHPPAQVNISKAILLGVILGGLIIFGVNLIVILSVACHRHLSVTHYYI 65
 QY 60 ANLTADLLYCTLLQPFSDVTYHLHWRTGATFCRVFGLLLFASNSVSIITLCLIALGRY 119
 Db 66 VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISIDRY 125
 QY 120 LLIAHPKLPQVFSAGKIVLALVSTWVG-VASFAPLWPIYILVP---VVTCTCFDRIRG 175
 Db 126 IGVSYPLRYPTIVTQRRGVRLLCVWALSIVISIGPLFGWRQQAPEDETIC-----QINE 180
 QY 176 RPYTTILMGI-YFVLGLSSVGIFYCLIHQVRAQAAL-----DQYKLRQASIH 223
 Db 181 EPGYVLFSAIGSFYVPLTIILVMYCRVYIVAKRESGLKTDKSDSEQVTLR---IH 237
 QY 224 SNHVARTDEAMPGRFQELDSRLASGPGSEGISSEPVSAATTQLEGDSSEVGDQINSKRA 283
 Db 238 RKNV-----PAEG---SGVSSAKNKT-----HFSVRL 262
 QY 284 KQMAEKSPPEASAKAQPIKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNLILDA 343
 Db 263 KFSREK-----KAAKTLGIIVGCVFLCWLPPFFLVMPFGS 296
 QY 344 ---RVQAPRVVHMLAANLTWNLGNCINPVLVYAMNRQFQAYGSI-----LKRGPSPHRL 395
 Db 297 FFPNFKPETVFKIVFWLGYNLSCINPIIYPCSSQEFKAFQNVLRIOCLRRRQSSKHAL 356
 RESULT 14
 Q8BV77 PRELIMINARY; PRT; 466 AA.
 AC Q8BV77;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adrenergic receptor.
 GN ADRA1A.
 RA Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=22354683; PubMed=12466851;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RL Nature 420:563-573(2002).
 DR EMBL; AK085653; BAC39495.1; -.
 DR MGD; MGI:104773; Adra1a.
 DR GO; GO:0008217; P:regulation of blood pressure; IMP.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOODOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 SQ SEQUENCE 427 AA; 47515 MW; 3810E9D5F5A09317 CRC64;
 Query Match 14.1%; Score 288.5; DB 11; Length 427;
 Best Local Similarity 23.1%; Pred. No. 9.2e-16;
 Matches 97; Conservative 78; Mismatches 148; Indels 97; Gaps 14;
 QY 3 NSSDANFSCYHESVLYGYRYVAVSWGVVVA---VTGTGNNVLTLLALAIQPKLRTFNLLI 59
 Db 7 NASEGS-NCTHPPAQVNISKAILLGVILGGLIIFGVNLIVILSVACHRHLSVTHYYI 65
 QY 60 ANLTADLLYCTLLQPFSDVTYHLHWRTGATFCRVFGLLLFASNSVSIITLCLIALGRY 119
 Db 66 VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISIDRY 125
 QY 120 LLIAHPKLPQVFSAGKIVLALVSTWVG-VASFAPLWPIYILVP---VVTCTCFDRIRG 175
 Db 126 IGVSYPLRYPTIVTQRRGVRLLCVWALSIVISIGPLFGWRQQAPEDETIC-----QINE 180
 QY 176 RPYTTILMGI-YFVLGLSSVGIFYCLIHQVRAQAAL-----DQYKLRQASIH 223
 Db 181 EPGYVLFSAIGSFYVPLTIILVMYCRVYIVAKRESGLKTDKSDSEQVTLR---IH 237
 QY 224 SNHVARTDEAMPGRFQELDSRLASGPGSEGISSEPVSAATTQLEGDSSEVGDQINSKRA 283
 Db 238 RKNV-----PAEG---SGVSSAKNKT-----HFSVRL 262
 QY 284 KQMAEKSPPEASAKAQPIKGARRAPDSSEFGKVTMCFVFLCFALSYPFLNLILDA 343
 Db 263 KFSREK-----KAAKTLGIIVGCVFLCWLPPFFLVMPFGS 296
 QY 344 ---RVQAPRVVHMLAANLTWNLGNCINPVLVYAMNRQFQAYGSI-----LKRGPSPHRL 395
 Db 297 FFPNFKPETVFKIVFWLGYNLSCINPIIYPCSSQEFKAFQNVLRIOCLRRRQSSKHAL 356
 RESULT 14
 Q8BV77 PRELIMINARY; PRT; 466 AA.
 AC Q8BV77;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adrenergic receptor.
 GN ADRA1A.
 RA Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=22354683; PubMed=12466851;

